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Perfect score:
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

5: /cgn2_6/ptodata/2,

6: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
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US-08-834-033A-2
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US-08-834-033A-15
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US-08-834-033A-17
US-08-834-033A-7
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US-08-834-033A-7
US-08-834-033A-17
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		121	121	127.5	128.5	128.5	128.5	130.5	130.5	136.5	136.5	141	141	141	184.5	184.5	184.5	196.5	196.5
		4.9	4.9	5.2	5.2	5.2	5.2	5.3	5.3	5.5	5.5	5.7	5.7	5.7	7.5	7.5	7.5	8.0	8.0
		104	104	382	125	125	125	155	155	186	186	87	87	87	143	143	143	131	131
	ALIGNMENTS	3 US-09-178-881-5	2 US-08-801-972-5	3 US-08-811-177A-2	4 US-09-363-574-8	3 US-08-834-033A-9	2 US-08-834-655-8 ·	3 US-09-178-881-1	2 US-08-801-972-1	3 US-08-834-033A-13	2 US-08-833-610-3	4 US-09-363-574-10	3 US-08-834-033A-11	2 US-08-834-655-10	4 US-09-363-574-11	3 US-08-834-033A-12	2 US-08-834-655-11	4 US-09-363-574-9	3 US-08-834-033A-10
		Sequence 5, Appli	Sequence 5, Appli	Sequence 2, Appli	Sequence 8, Appli	Sequence 9, Appli	Sequence 8, Appli	Sequence 1, Appl1	Sequence 1, Appl1	Sequence 13, Appl	Sequence 3, Appli	Sequence 10, Appl	Sequence 11, Appl	Sequence 10, Appl	Sequence 11, Appl	Sequence 12, Appl	Sequence 11, Appl	~	Sequence 10, Appl

US-08-834-655-2

Sequence 2, Application US/08834655 Patent No. 5968809

GENERAL INFORMATION:

APPLICANT:

KNUTZON, DEBORAH MURKERJI, PRADIP

APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURNOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

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; LENGTH: 457 amino
; TYPE: amino acid
; STRANDEDNESS: not
; TOPOLOGY: linear
; MOLECULE TYPE: pepti
US-08-834-655-2
                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94306
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
CLASSIFICATION: 435
Query Match
Best Local Similarity
Matches 457; Conserv
                                                                                                                                                                                                 TELEX: N/A
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE
TELECOMMUNICATION INFORMATION:
TELECHONE: (650) 328-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
ADDRESSEE: RAE-VENTER LAW GROUP, P.O. BOX 60039
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 260 SHE
CITY: PALO ALTO
STATE: CA
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                                                                                                                                                                                                                                                                                    (650) 328-4477
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                                                                                                                                                            not relevant
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Score 2465; DB 2;
Pred. No. 1.8e-270;
Mismatches 0;
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Conservative

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Gaps

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US-08-834-033A-2
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                                                                                                                       SOFTWARE: WORDPERFECT 5.7

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION
THE TOWN INFORMATION INF
                                            INFORMATION FOR SEQ ID NO:
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APPLICANT:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
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APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
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                                                                                                   TELEX:
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STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: I
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Best Local S
Matches 457
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APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                    COUNTRY: USA
ZIP: 94111
                                                                                                                               CITY: SAN FRANCISCO
STATE: CA
                                                                                                                                                              ADDRESSEE: LIMBACH AND LIMBACH L.L.P. STREET: 2001 FERRY BUILDING
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APPLICATION NUMBER:
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Best Local
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ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEPHONE: (415) 433-8716
                                                                                                                                                                                                GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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MOLECULE TYPE:
)9-363-574-2
            APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS: AND COMPOSITION
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSP
MUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVE, P.O. BOX 60039
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LENGTH: 457 amino acids
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STREET:
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PALO ALTO
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HUANG, YUNG-SHENG
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                                                             METHODS AND COMPOSITIONS FOR SYNTHESIS OF LONG CHAIN POLY-UNSATURATED FATTY AGE 12
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Pred. No. 1.8e-270;
Mismatches 0;
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Best Local Similarity
Matches 456; Conserv
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LENGTH: 457 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)328-4400
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NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,7
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APPLICATION NUMBER: US,
FILING DATE: 11-APR-199
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               421 KKYNVRYHTTGMIEGTAEVFSRLNEVSKAASKMGKAQ 457
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TOPOLOGY: lir
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                                                         EEAVDMDFFTKQIITGRDVHPGLFANWFTGGLNYQIEHHLFPSMPRHNFSKIQPAVETLC
                                                                                                                                       SLVEQLSLAMHWTWYLATMFLFIKDPVNMLVYFLVSQAVCGNLLAIVESLNHNGMPVISK 360
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KKYNVRYHTTGMIEGTAEVFSRLNEVSKAASKMGKAQ
                                                                                                                             SLVEQLSLAMHWTWYLATMFLFIKDPVNMLVYFLVSQAVCGNLLAIVFSLNHNGMPVISK
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Pred. No. 1.9e-269;
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US-08-834-033A-14

Sequence 14, Application US/08834033A Patent No. 6075183
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH

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MOLECULE TYPE: US-08-834-033A-14
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TELEX: N/A
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
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Best Local Similarity 99.8%;
Matches 456; Conservative
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NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAE
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 143-4150
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APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/834,033A FILING DATE: 11-APR-1997 CLASSIFICATION: 800
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                  SLVEQLSLAMHWTWYLATMFLFIKDPVNMLVYFLVSQAVCGNLLAIVFSLNHNGMPVISK 360
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                  EEAVDMDFFTKQIITGRDVHPGLFANWFTGGLNYQIEHHLFPSMPRHNFSKIQPAVETLC 420
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Pred. No. 1.9e-269;
0; Mismatches 1; Indels
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US-08-834-655-5
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                               Matches
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
NAME: RAE-VENTER, BARBARA
NAME: RAE-VENTER, BARBARA
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
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LENGTH: 355 amino acids
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REFERENCE/DOCKET NUMBER: CGNE.124.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
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APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
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ZIP: 94306
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                                 PDIDTHPLLTWSEHALEMFSDVPDEELTRWWSRFWVLNQTWFYFPILSFARLSWCLQSIL
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LLAIVFSLNHNGMPVISKEEAVDMDFFTKQIITGRDVHPGLFANWFTGGLNYQIEHHLFP
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260 SHERIDAN AVENUE, P.O. BOX
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Best Local :
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ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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                                             103 EVRKLRTLEQSLGYYDSSKAYYAFKVSFNLCIWGLSTVIVAKWGQTSTLANVLSAALLGL 162
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               FVLPNGQAHKPSGARVPISLVEQLSLAMHWTWYLATMFLFIKDPVNMLVYFLVSQAVCGN
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HUANG, YUNG-SHENG
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                                                                                                                                                                                                        Query Match
Best Local
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
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APPLICATION NUMBER: US/09/363,57
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
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                                                                                                                                             103 EVRKLRTLEQSLGYYDSSKAYYAFKVSFNLCIWGLSTVIVAKWGQTSTLANVLSAALLGL 162
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121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
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                                                                                                                            1 EVRKLRTLFQSLGYYDSSKAYYAFKVSFNLCIWGLSTVIVAKWGQTSTLANVLSAALLGL 60
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PDIDTHPLLTWSEHALEMFSDVPDEELTRMWSRFMVLNQTWFYFPILSFARLSWCLQSIL
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241 LLAIVFSLNHNGMPVISKEEAVDMDFFTKQIITGRDVHPGLFANWFTGGLNYQIEHHLFP

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SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 32,750
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)328-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/833,610 FILING DATE: 11-APR-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVE, P.O. BOX 60039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
                                                                                                                                                                                                                                      MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 84
                                                                                                                                  Local Similarity
mes 136; Conserv
                                                                                                                                                                                                                                                    TOPOLOGY: linear
                             95 IKNDDFAAEVRKLRTLFQSLGYYDSSKAYYAF-----KVSFNLCIWGLSTVIVAKWGQT 148
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                                                                                 IDNKYYDVREFVPDHPGGSVILTHV-GKDGTDVFDTFHPEAAWETLANFYVGDIDESDRD 94
YSVSEVSKVYRKLVFEFSKMGLYD-KKGHIMFATLCFIAMLFAMSVYG---VLFCE---- 135
                                                              IQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAFVAFHPASTWKNLDKFFTG---YYLKD
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5. 5972664
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                                                                                                                                                                                                                                                                                                                                                                     : (650)328-4400
(650)328-4477
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HUANG, YUNG-SHENG
                                                                                                                                  Conservative
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                                                                                                                                                                                                                                   peptide
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                                                                                                                                               Score 514.5; DB 2
Pred. No. 1.5e-49;
                                                                                                                                  Mismatches 183;
                                                                                                                                                               DB 2;
                                                                                                                                                                 Length 446;
                                                                                                                                  Indels
                                                                                                                                  41;
                                                                                                                              Gaps
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; TOPOLOGY: 1; MOLECULE TYPE: US-08-834-033A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6075183
GENERAL INFORMATION:
                                                                                                                                     INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 38,651
TELECOMMUNICATION INFORMATION:
TELEPHONE: //15 / 17
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                                                                                              SEQUENCE CHARACTERISTICS: LENGTH: 446 amino acid
                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R
                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
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CLASSIFICATION:
                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                      NAME: WARD, MICHAEL R. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                              amino acid
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                                                                                              446 amino acids
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HUANG, YUNG-SHENG
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                                                                                                                                                                             (415) 433-8716
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                                        linear
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                  peptide
                                                        not relevant
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US-08-366-779-5
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Patent No. 5614393
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                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                    CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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           REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 30-DEC-1994
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                                                                NAME: Presser, Leopold REGISTRATION NUMBER: 1
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TELEFAX:
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MT 417
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                                                                                                                                                                                                                                                                                     11530
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                                                                                                                                                                                                                                                                                                                      New York
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WENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY
                                                                                                                                                                                                                                                                                                  United States
 (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Freyssinet, Georges L.
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Nuccio, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-789-936-5
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08789936 Patent No. 5789220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 135;
                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acid
                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS: ADDRESSEE: Scully, S
                                                                                                                                                                                                                                                    APPLICANT: Nunberg, Andrew N.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    446
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                                                                                                                                         COUNTRY:
                                                                                                                                                                            STREET: 400 Garden
CITY: Garden City
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                                                                                                                                                             STATE:
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 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NWFTGGLNYQIEHHLFPSMPRHNFSKIQPAVETLCKKYNVRYHTTGMIEGTAEVFSRLNE 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GERIMFVIASLSVTG-MQQVQFSLNHFSSSVYVGKPKG--NNWFEKQTDGTLDISCPPWM 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HNAHHIACNSLEYDPDLQYIPFLVVSSKFFGSLTSHFYEKRLTFDSLSRFFVSYQHWTFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVLVHLFSGCLMGFLWIQSGWIGHDAGHYMYVSDSRLNKFMGIFAANCLSGISIGWWKWN 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STLANVLSAALLGLFWQQCGWLAHDFLHHQVFQDRFWGDLFGAFLGGVCQGFSSSWWKDK 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIMCAARLNMYVQSLIMLL-----TKRNVSYRAQELLGCLVFSIWY-PLLVSCLPNW 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PILSFARLSWCLQSILFVLPNGQAHKPSGARVPISLVEQLSLAMHWTWYLATMFLFIKDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YSVSEVSKDYRKLVFEFSKMGLYD-KKGHIMFATLCFIAMLFAMSVYG---VLFCE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAFVAFHPASTWKNLDKFFTG---YYLKD 83
                                                                                                                            11530
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                                                                                                                                                          New York
                                                                                                                                                                                               E: Scully, Scott, Murphy & Presser 400 Garden City Plaza
                                                                                                                                           United States
                                                                                                                                                                                                                                                                                                                                                               Reddy, Avutu S
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32.0%;
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US/08/789,936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 183;
                                   Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                       #
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ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: FILING DATE: 30-DEC

30-DEC-1994

08/366,779

PRIOR APPLICATION DATA:

CLASSIFICATION:

FILING DATE:

28-JAN-1997

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                                                                                                                                                                                                                                                                        RESULT 13
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Best Local S
Matches 135
                                                                                                                                                                                                           Sequence 7, Applic Patent No. 5968809
                                                                                                                                                                                        GENERAL INFORMATION:
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               APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY AC
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 8383ZYXW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                       416 MT 417
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                                                                                                                                                                                                                                                                                                                                                                                                                     364 DWFHGGSQFQIEHHLFPKMPRCNLRKISPYVIELCKKHNLPYNYAS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 HNAHHIACNSLEYDPDLQYIPFLVVSSKFFGSLTSHFYEKRLTFDSLSRFFVSYQHWTFY 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 32.0 nes 135; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            VS 447
                                                                                                                                                                                                                                                                                                                                                                                                                                             NWFTGGLNYQIEHHLFPSMPRHNFSKIQPAVETLCKKYNVRYHTTGMIEGTAEVFSRLNE 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HNTHHAAPNVHGEDPDIDTHPLLTWSEHAL-EMFSDVPDEELT-RMWSRFMVLNQTWFYF 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STLANVLSAALLGLFWQQCGWLAHDFLHHQVFQDRFWGDLFGAFLGGVCQGFSSSWWKDK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIMCAARLNMYVQSLIMLL-----TKRNVSYRAQELLGCLVFSIWY-PLLVSCLPNW 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IKNDDFAAEVRKLRTLFQSLGYYDSSKAYYAF-----KVSFNLCIWGLSTVIVAKWGQT 148
                                                                                                                                                                                                                               Application US/08834655
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                                                                                                                                                                                                                                                                                                                                                                                                                     ---FSKANE 415
                                       ACIDS IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41;
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                                                                                                                                                                                                                                    Sequence 8, Application US/08834033A Patent No. 6075183
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                      GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: N/A INFORMATION FOR SEQ ID NO:
                                      TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (650) 328-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   229 TIDISCRSYMDWFFGGLQFQLEHH 252
                                                                                                                                                                                                                                                                                                                                                                                                           376 GRDVHPGLFANWFTGGLNYQIEHH 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 FIKDPVNMLVYFLVSQAVCGNLLAIVFSLNH-----NGMPVISKEEAVDMDFFTKQIIT 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 HFTYYPVNCFGRINLFIQTFLLLF------SKREVPDRALNFAGILVFWTWFPLLVSC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 TSTLANVLSAALLGLFWQQCGWLAHDFLHHQVFQDRFWGDLFGAFLGGVC-QGFSSSWWK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 DKHNTHHAAPNVHGEDPDIDTHPLLTWSEHALEMFSDVP----DEELT-RMWSRFMVLNQ 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 WTHNAHHLACNSLDYDPDLQHIPVFAVS---TKFFSSLTSRFYDRKLTFGPVARFLVSYQ 125
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TOPOLOGY: lir
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OPERATING SYSTEM: PC-DOS/MS-DOS
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 TSVFAHQIAAALLGLLWIQSAYIGHDSGHYVIMSNKSY-NRFAQLLSGNCLTGISIAWWK 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 32 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0
FILING DATE: 11-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: RAE-VENTER LAW GROUP, P.C. STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TWFYFPILSFARLSWCLQSILFVLPNGQAHKPSGARVPISLVEQLSLAMHWTWYLATMFL 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPNWPERF--FFVFTSFTVTALQHIQFTLNHFAADVYVGPPTGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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LIMBACH AND LIMBACH, L.L.P.
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                                                                IN PLANTS
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STREET: 2001 FERRY I

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US-09-363-574-7; Sequence 7, Application US/09363574; Patent No. 6136574
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                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
                                       TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/834,033A FILING DATE: 11-APR-1997 CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION: NAME: WARD, MICHAEL R. REGISTRATION NUMBER: 38,651 REGESTRATION NUMBER: 38,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 TSTLANVLSAALLGLFWQQCGWLAHDFLHHQVFQDRFWGDLFGAFLGGVC-QGFSSSWWK 200
                                                                                                                                                                                                                                                                                                                                                                             229 TIDISCRSYMDWFFGGLQFQLEHH 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 TWFYFPILSFARLSWCLQSILFVLPNGQAHKPSGARVPISLVEQLSLAMHWTWYLATMFL 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 DKHNTHHAAPNVHGEDPDIDTHPLLTWSEHALEMFSDVP----DEELT-RMWSRFMVLNQ 261
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5 1
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                       ADDRESSEE:
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HUANG, YUNG-SHENG
THURMOND, JENNIFER
CHAUDHARY, SUNITA
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Best Local Similarity 30.3%;
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INFORMATION FOR SEQ ID NO: 7:
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ATTORNEY/AGENT INFORMATION:
ATTORNEY WARD, MICHAEL R.
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                            178
                                                                                                                                                                                                                                                                                                                                   148 TSTLANVLSAALLGLFWQQCGWLAHDFLHHQVFQDRFWGDLFGAFLGGVC-QGFSSSWWK 206
                                                                                                                                                      126 HETTYYPVNCFGRINLFIQTFLLLF-----SKREVPDRALNFAGILVFWTWFPLLVSC 177
                                                                                                              322 FIKDPVNMLVYFLVSQAVCGNLLAIVFSLNH-----NGMPVISKEEAVDMDFFTKQIIT 375
                                                                                                                                                                                          262 TWFYFPILSFARLSWCLQSILFVLPNGQAHKPSGARVPISLVEQLSLAMHWTWYLATMFL 321
                                                                                                                                                                                                                                                                     207 DKHNTHHAAPNVHGEDPDIDTHPLLTWSEHALEMFSDVP----DEELT-RMWSRFMVLNQ 261
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                      LPNWPERF--FEVFTSFTVTALQHIQFTLNHFAADVYVGPPTGS-----DWFEKQAAG
TIDISCRSYMDWFFGGLQFQLEHH
                                      GRDVHPGLFANWFTGGLNYQIEHH 399
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amino acid
DEDNESS: not relevant
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Pred. No. 8.3e-25;
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Search completed: August Job time: 204 sec 9, 2001, 20:25:05

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
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A_Geneseq_0601:*

1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
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3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

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Result	200	Query) } + F		COMPANY	
			111111	•		
1	2465	100.0	457	19	AAW84137	A delta-6 desatura
2	2465	100.0	457	20	AAW95504	Mortierella alpina
ω	2465	100.0	457	21	AAY92599	M. alpina delta-6
4	2465	100.0	457	21	AAY56045	Fungal delta6-desa
5	2465	100.0	457	22	AAB31684	Amino acid sequenc
6	2456	99.6	457	20	AAW85121	A delta-6 desatura
7	1930	78.3	355	19	AAW84139	Desaturase enzyme
80	873	35.4	520	22	AAB46440	C. purpureus delta
9	841.5	34.1	483	22	AAB46435	C. purpureus delta
10	841.5	34.1	483	22	AAB46436	C. purpureus delta
11	818	33.2	525	21	AAY51354	Protein b5pp with

45	44	43	42	41	40	39	38	37	36	<u>3</u> 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
478.5	478.5	478.5	478.5	478.5	478.5	478.5	493	497.5	502	502.5	508.5	514.5	515.5	518.5	518.5	518.5	521	521	522	522	523	523.5	524.5	524.5	534.5	537	549	5	•	2	629	631	\mathbf{L}
19.4	19.4	•	19.4	19.4	19.4	•	•	•	•	•	•	•					•	•	•	•	•	•	•	•		•		•	•	•	•	25.6	•
753	752	746	746	445	445	432	469	449	449	450	444	446	448	448	448	448	517	449	449	449	462	444	444	444	458	473	448	443	454	4	4	422	N
20	21	20	19	21	21	21	21	21	21	21	21	20	21	20	19	17	21	21	21	21	21	21	22	21	21	21	21	20	21	21	20	21	22
AAW95514	6	AAW85135	AAW84156	22	AAY97540	AAY95446	AAY71555	AAG29290	AAY51333	AAY71554	AAB41998	AAW85122	AAY51349	AAW98130	AAW67471	AAR98455	AAG07391	AAG07392	AAY51334	AAG53861	AAY71552	AAY97538	AAB31686	AAY95445	AAY51348	AAY51353	AAY71551	AAY17751	AAY51355	672		S)	AAB46810
Amino acid sequenc	Human desaturase	A desaturase enzym	Human desaturase		Human fatty acid	Human delta-5-des	Wheat sphingolipid	Arabidopsis thalia	Ω.	Soybean sphingoli	×	A delta-6 desatur	Sunflower HADES pr	Borage delta-6 des	delta-	Borage delta-6-des				Arabidopsis thalia	0	~	Amino acid sequenc	Human delta-5-desa	Sphingolipid desa		Florida bitterbush	norhabd	rotein 25k	. elegans	. elegans delt	racili	. patens de

ALIGNMENTS

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AAW84137
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                                                                                                                                                                                                                                                                                                                                                                          Fatty acid; delta-6 desaturase; polyunsaturated fatty acid; mainutrition; inflammation; rheumatoid arthritis; asthma; psoriasis; cancer; diabetes; eczema; platelet regation; vasodilation; cholesterol level; endometriosis; premenstrual syndrome; myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis; acute respiratory syndrome; hypertension; inflammatory skin disorder.
                                       Chaudhary S, Thurmond J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A delta-6 desaturase enzyme.
WPI; 1998-594582/50.
                                                                                                                                                                                                                                                        22-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW84137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW84137 standard; Protein;
                                                                                                                                                                  11-APR-1997;
                                                                                                                                                                                                                                                                                                WO9846763-A1
                                                                                                                                                                                                                                                                                                                                         Mortierella alpina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-FEB-1999
                                                                                                     (ABBO ) ABBOTT LAB.
(CALJ ) CALGENE LLC.
                                                                                                                                                                                                            10-APR-1998;
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                                                         Huang Y,
                                                                                                                                                                    97US-0834655
                                                                                                                                                                                                            98WO-US07126
                                                             Knutzon D,
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                                                             Leonard AE,
                                                             Mukerji P;
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SXCCCCCCCCCCCCCCCCX PX PTTX R

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CC The present sequence represents a Mortierella alpina fatty acid delta-6 CC desaturase enzyme. The enzyme sequence is used in the methods of CC the invention. The specification describes methods for desaturating a CC fatty acid and for producing a desaturated fatty acid by expressing CC increased levels of a desaturate. The present desaturase is an enzyme CC which introduces a double bond carbons 6 and 7 from the carboxyl end of CC a fatty acid molecule. The enzyme can be used for desaturating fatty CC acids. The enzyme can be used to produce polyunsaturated fatty acids, CC which can be used for treating malnutrition, in pharmaceutical CC compositions, in cosmetics or in animal feed. The polyunsaturated fatty cids caids can be used for treating e.g. restenosis after angioplasty, CC inflammation, rheumatoid arthritis, asthma, psoriasis, cancer, diabetes CC or eczema or reduce blood pressure. They can also be used to inhibit conhibit proliferation of vessel wall smooth muscle and fibrous tissue, CC inhibit proliferation of vessel wall smooth muscle and fibrous tissue, CC caused by non-steroidal anti-inflammatory drugs, prevent or treat CC and chronic fatigue after viral infections, treat myalgic encephalomyelitis CC caused by non-steroidal anti-inflammatory drugs, multiple CC sclerosis, acute respiratory vendrome, hyperfension and inflammatory acids infammatory and inflammatory acids and infammatory acids in the control of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
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421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSDVPDEELTRMWSRFMVLNQTWFYEPILSFARLSWCLQSILFVLPNGQAHKPSGARVPI 300
                           KKYNVRYHTTGMIEGTAEVFSRLNEVSKAASKMGKAQ
                                                                                                                                                                              EEAVDMDFFTKQIITGRDVHPGLFANWFTGGLNYQIEHHLFPSMPRHNFSKIQPAVETLC
                                                                                                                                                                                                                                                                                      {\tt slveqlslamhwtwylatmflfikdpvnmlvyflvsqavcgnllaivfslnhngmpvisk}
                                                                                                                                                                                                                                                                                                                             SLVEQLSLAMHWTWYLATMFLFIKDPVNMLVYFLVSQAVCGNLLAIVFSLNHNGMPVISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QDRFWGDLFGAFLGGVCQGFSSSWWKDKHNTHHAAPNVHGEDPDIDTHPLLTWSEHALEM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kayyafkvsfnlciwglstvivakwgqtstlanvlsaallglfwqqcgwlahdflhhqvf 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAYYAFKVSFNLCIWGLSTVIVAKWGQTSTLANVLSAALLGLFWQQCGWLAHDFLHHQVF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gkdgtdvfdtfhpeaawetlanfyvgdidesdrdiknddfaaevrklrtlfqslgyydss 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKDGTDVFDTFHPEAAWETLANFYVGDIDESDRDIKNDDFAAEVRKLRTLFQSLGYYDSS 120
                                                                                                                                   \tt eeavdmdfftkqiitgrdvhpglfanwftgglnyqiehhlfpsmprhnfskiqpavetlc
                                                                                                                                                                                                                                                                                                                                                                                                                                             fsdvpdeeltrmwsrfmvlnqtwfyfpilsfarlswclqsilfvlpngqahkpsgarvpi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         457;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   c tatigue after viral infections, treat AIDS, multiple acute respiratory syndrome, hypertension and inflammatory skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   457
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Pred. No. 1.1e-245;
); Mismatches 0;
                                                                 457
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                                                                                                                                                                                                                                                                                          360
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0;

RESULT AAW95504 ID AAW9

N

Query Match Matches 457; Best Local Similarity

Conservative

0,:

Indels Length 457;

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Gaps

0

100.0%;

Score 2465; DB 20; Pred. No. 1.1e-245; Mismatches

457

AAW95504 standard; peptide; 457 AA

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This represents a Mortierella alpina delta 6 desaturase. The invention crelates to a nucleic acid construct that contains at least one of the nucleotide sequences (AAN/0089) to AAA/00891) encoding M. alpina delta 6, delta 12 and delta 5 desaturases (AAN/0504) to AAN/0506) respectively, coupled to an expression control sequence functional in plants. Recombinant plant cells containing at least one DNA encoding a M. alpina delty acid desaturase (FAD), can be used for the production of plants containing them are used to produce oils such as linoleic acid, containing them are used to produce oils such as linoleic acid, arachidonic acid, gamma-linolenic acid, dihomo-gamma-linolenic acid, arachidonic acid and eicosapentaenoic acid (EPA). These plant oils are used: (1) to treat malnutrition; (ii) in infant feeding formulas, or clietary supplements or substitutes, for use in humans or animals; (iii) for treating disorders associated with inadequate consumption or production of PUFA (or their metabolites such as prostaglandins), e.g. restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis, psoriasis, osteoporosis, cancer, eczema, diabetes; (1) as cosmetics, and (1) as animal feeds. Fragments of the DNA are used as probes to isolate
                                                      related coding sequences. Recombinant plants can produce high yields of PUFA, since new pathways can be created and unwanted ones suppressed. Plants can be engineered to express oils of particular PUFA composition, e.g. one similar to that in human milk, and product recovery is simpler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid construct able to express fatty acid desaturase in plants - useful in human or animal nutrition, as cosmetics and therapeutically, e.g. for restenosis, cancer and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic; stearidonic acid; eicosapenteaenoic acid; minutrition; stearidonic acid; eicosapenteaenoic acid; minutrition; inflammation; dietary supplement; prostaglandin; restenosis; angioplasty; inflammation; rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Fig 3A-E; 210pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chaudhary S, Thurmond J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-APR-1997;
11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diabetes; cosmetic; animal feed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ABBO ) ABBOTT LAB.
(CALJ ) CALGENE LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mortierella alpina delta 6 desaturase.
                                   e.g. fish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Huang
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97US-0833610.
97US-0834033.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recombinant; fatty acid desaturase; FAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Knutzon D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leonard AE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         osteopathic; cytostatic; antidiabetic; dermatological; gynecological; anti-HIV; neuroprotective; hypotensive; nephrotropic; vasodilator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transgenic insect cell; polyunsaturated long chain fatty acid; antiinflammatory; antirheumatic; antiasthmatic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY92599 standard;
                       (ABBO ) ABBOTT
                                                                     05-OCT-1998;
                                                                                                                                                                                                          WO200020602-A2
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                               KKYNVRYHTTGMIEGTAEVFSRLNEVSKAASKMGKAQ
                                                                                                                            {\tt slveqlslamhwtwylatmflfikdpvnmlvyflvsqavcgnllaivfslnhngmpvisk}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    feed formulations. The long chain PFAs can be used in nutritional formulations, cosmetic formulations or animal feed formulations. The products can also be used for producing transgenic animals which can used for producing essential FAs which can be used for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method of generating novel compositions comprising animal cells producing essential fatty acids (FAs). The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Producing essential fatty acids and long-chain acids, for use in nutritional, animal feed and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kopchick JJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fungal delta6-desaturase protein sequence
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); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polyunsaturated fatty
medical formulations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              457;
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RESULT
AAB31684
ID AAB3
XX
AC AAB3
XX
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                       polynucleotide sequence was used to trasfect mammalian cells, to produce animal cells expressing a desaturase gene and/or an elongase gene. Compositions comprising cells of the invention are useful for synthesising essential fatty acids, their derivatives or downstream products, as well as altered levels of long-chain polyunsaturated fatty acids and elcosanoids. The compositions are useful in nutritional formulae, e.g. infant formula, dietary supplements or dietary substitutes for both humans and animals. The compositions are also useful in cosmetic or animal feed formulations. Furthermore, the compositions may also be used as fat free media or as research reagents.
                                                                                                                                                                                                                                 New compositions comprising cells that express desaturases and elongases, for synthesizing essential fatty acids or long-chain polyunsaturated fatty acids, used in nutritional, cosmetic or a
Sequence
                                                                                                                                                                                                                                                                                                                                 Kopchick JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200104636-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mortierella alpina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        delta6 desaturase; desaturase gene; elongase gene; fatty acid;
elcosanoid; nutrition; infant formula; dietary supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB31684 standard; Protein; 457
                                                                                                                                                                 The present sequence represents a delta6 desaturase.
                                                                                                                                                                                                                                                                                                                                                             (UYOH-) UNIV OHIO.
                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUL-2000; 2000WO-US19011.
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                                                                                                                                                                                                                                                                                          AAF25234
 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence of a fungal delta6 desaturase
                                                                                                                                                                                           Fig 9; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                 Kelder
 AA;
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                                                                                                                                                                 The desaturase
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Query Match
Best Local Similarity
Matches 457; Conserv

100.0%; ilarity 100.0%; Conservative

0

Mismatches

0.

Indels Length

Gaps

0

Score 2465; DB 22; Pred. No. 1.1e-245;

DB 22;

457; 0;

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RESULT
AAW85121
ID AAW8
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                                                                                                                                                                               Thurmond J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis; cancer; diabetes; eczema; platelet aggregation; vasodilation; cholesterol level; endometriosis; premenstrual syndrome; myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW85121 standard;
                                         New nucleic acid encoding delta5 and other desaturase enzymes useful in production of oils of increased arachidonic acid coused, e.g. for treating cancer, as foods, animal feeds and coused, e.g. for treating cancer, as foods, animal feeds and coused, e.g. for treating cancer, as foods, animal feeds and couper to the contract of the 
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                                                                                                                                                                                                                                             (ABBO ) ABBOTT LAB. (CALJ ) CALGENE LLC.
                                                                                                                                                                                                                                                                                                                                                         10-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KAYYAFKVSFNLCIWGLSTVIVAKWGQTSTLANVLSAALLGLFWQQCGWLAHDFLHHQVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKDGTDVFDTFHPEAAWETLANFYVGDIDESDRDIKNDDFAAEVRKLRTLFQSLGYYDSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAAAPSVRTFTRAEVLNAEALNEGKKDAEAPFLMIIDNKVYDVREFVPDHPGGSVILTHV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acid; delta-6 desaturase; polyunsaturated fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    respiratory syndrome; hypertension;
  Pages 95-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                             97US-0833610
                                                                                                                                                                                                                                                                                                                                                         98WO-US07422
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                                                                                                                                                                                                      Knutzon
153pp;
  English
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                                                                                                                                                                                                   Mukerji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid;
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The present sequence represents a fatty acid delta-6 desaturase enzyme. The specification describes methods for desaturating a fatty acid and for producing a desaturated fatty acid by expressing increased levels of a desaturase. The present desaturase is an enzyme which introduces a double bond carbons 6 and 7 from the carboxyl end of a fatty acid molecule. The enzyme can be used for desaturating fatty acids. The enzyme can be used for treating malnutrition, in pharmaceutical compositions, be used for treating malnutrition, in pharmaceutical compositions, in cosmetics or in animal feed. The polyunsaturated fatty acids can be used for treating e.g. restenosis after angioplasty, inflammation, reduce blood pressure. They can also be used to inhibit platelet aggregation, cause vasodilation, lower cholesterol levels, inhibit proliferation of vessel wall smooth muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding and other side effects caused by non-steroidal anti-inflammatory drugs, prevent or treat endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis and chronic fatigue after viral infections, treat along multiple
                                                                                    sclerosis,
                                                                              acute respiratory syndrome, hypertension and inflammatory skin
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Sequence 457 AA,

Query Match Best Local

Similarity

99.6%;

DB 20;).2e-245;

Length

457;

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RESULT
AAW84139
ID AAW8
XX
AC AAW8
AX
DT 15-F
XX
DE Desa
XX
Fatt
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                                                                                                                                                                                                                                                                                                                                                                   KKYNVRYHTTGMIEGTAEVFSRLNEVSKAASKMGKAQ
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                                                                                                                                                                             EEAVDMDFFTKQIITGRDVHPGLFANWFTGGLNYQIEHHLFPSMPRHNFSKIQPAVETLC
                                                                                                                                                                                                        {\tt slveqlslamhwtwylatmflfikdpvnmlvyflvsqavcgnllaivfslnhngmpvisk}
                                                                                                                                                                                                                  SLVEQLSLAMHWTWYLATMELFIKDPVNMLVYFLVSQAVCGNLLAIVESLNHNGMPVISK
                                                                                                                                                                                                                                              QDRFWGDLFGAFLGGVCQGFSSSWWKDKHNTHHAAPNVHGEDPDIDTHPLLTWSEHALEM
                                                                                                                                                                  ee avd \texttt{m} df \texttt{ftkqiitgrdvhpglfanwftgglnyqiehhlfpsmprhnfskiqpavetlc}
                                                                                                                                                                                                                                                                                      \verb|gdrfwgdlfgaflggvcqgfssswwkdkhnthhaapnvhvedpdldthplltwsehalem||
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2456; D
Pred. No. 9.2e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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Fatty acid; desaturase; polyunsaturated fatty

acid;

Desaturase

enzyme

peptide sequence.

15-FEB-1999

(first entry)

AAW84139

AAW84139 standard;

Peptide;

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Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         increased levels of a desaturase. Desaturases can be used for desaturating fatty acids. The enzymes can be used for produce polyunsaturated fatty acids, which can be used for treating malnutrition, in pharmaceutical compositions, in cosmetics or in animal feed. The polyunsaturated fatty acids can be used for treating e.g. restenosis after angioplasty inflammation, rheumatoid arthritis, asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure. They can also be used to inhibit platelet aggregation, cause vasodilation, lower cholesterol levels, inhibit proliferation of vessel wall smooth muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding and other side effects caused by non-steroidal anti-inflammatory drugs, prevent or treat endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis and chronic fatigue after viral infections, treat AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated fatty acid desaturase enzymes - used for the production of polyunsaturated fatty acids for use in, e.g. pharmaceutical compositions, nutritional compositions, cosmetics or animal feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis; cancer; diabetes; eczema; platelet aggregation; vasodilation; cholesterol level; endometriosis; premenstrual syndrome; myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis; acute respiratory syndrome; hypertension; inflammatory skin disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a peptide derived from a desaturase enzyme. The specification describes methods for desaturating a fatty acid and for producing a desaturated fatty acid by expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Pages 101-102; 165pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-594582/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chaudhary S, Thurmond J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
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      343
                                                                      181
                                                                                                                                                                                            121
                                                                                                                            283
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                                                                                                                                                                                                                                                                                                                                                                                163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 EVRKLRTLFQSLGYYDSSKAYYAFKVSFNLCIWGLSTVIVAKWGQTSTLANVLSAALLGL 162
                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
LLAIVFSLNHNGMPVISKEEAVDMDFFTKQIITGRDVHPGLFANWFTGGLNYQIEHHLFP 402
                                                                                                                                                                                PDIDTHPLITWSEHALEMFSDVPDEELITRMWSRFMVLNQTWFYFPILSFARLSWCIQSIL 282
                                                                                                                                                                                                                                                                                                                                         FWQQCGWLAHDFLHHQVFQDRFWGDLFGAFLGGVCQGFSSSWWKDKHNTHHAAPNVHGED 222
                                                   evrklrtlfqslgyydsskayyafkvsfnlciwglstvivakwgqtstlanvlsaallgl 60
                                                                                                                                                                                                                                                                                                         fwqqcgwlahdflhhqvfqdrfwgdlfgaflggvcqgfssswwkdkhnthhaapnvhged 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0834655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders.
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100.0%;
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 Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1930; DB 19;
Pred. No. 1.2e-190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leonard AE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 355;
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34 MIIDNKVYDVREFVPDHPGGSVILTHVGKDGTDVFDTFHPEAAWETLANFYVGDIDESDR 93

Matches 185; Query Match

Conservative

68;

Score 873; DB 22; Pred. No. 2.5e-81; 8; Mismatches 134;

Length 520; Indels

42;

Gaps

10;

35.4%;

Local Similarity

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RESULT
AAB46440
ID AAB4
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                                       activity. The invention also describes (a) amino acid sequences encoded (b) (I); (b) an expression cassette (EC) containing (I) linked to one or comore regulatory sequences; (c) a vector containing (I) and EC; (d) (c) organisms containing (I), EC or the vectors of (c); (e) preparation of (c) consaturated fatty acids (A) or triglycerides (Mo) with increased content (c) of (A) by introducing (I) or EC into an oil-producing organism; (f) (c) proteins (IIa) of 172 as or 178 as (given in the specification); (g) (c) production of (A) or TG by using (Ia); and (h) (A) and TG produced by (c) method (g). (I) are used to produce transgenic plants (or other (c) organisms) that produce oils or triglycerides (TG) with increased content (c) unsaturated fatty acids (A) and to isolate related sequences by (c) method (g). (a) or TG containing them, are useful in human (c) nutrition (e.g. infant foods), animal feeds, pharmaceuticals and (c) completes expression of (II), resulting in oils with
Sequence
                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding delta6-acetylenase or desaturase, useful for producing plant oils with increased content of unsaturated fatty as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1999;
22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C. purpureus delta6-acetylenase/delta6-desaturase SEQ
                                                                                                                                                                                                                                                                                        polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase
                                                                                                                                                                                                                                                                                                          This invention describes a novel isolated nucleic acid (I) encoding
                                                                                                                                                                                                                                                                                                                                          Example 7; Page 57-59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heinz E,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid; transgenic plant; plant oil; triglyceride; nutrition; animal feed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-APR-2001
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                               increased
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMPRHNFSKIQPAVETLCKKYNVRYHTTGMIEGTAEVFSRLNEVSKAASKMGKAQ 457
                             content of saturated fatty acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stymne S,
 520 AA;
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99DE-1062409
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This invention describes a novel isolated nucleic acid (I) encoding polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase activity. The invention also describes (a) amino acid sequences encoded
                                                                        Nucleic acid encoding delta6-acetylenase or producing plant oils with increased content
                                                                                                                                                                               07-JUN-1999;
22-DEC-1999;
                                                                                                                                                                                                                                                                                                        Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid transgenic plant; plant oil; triglyceride; nutrition; animal
                                                                                                                                                                                                                                                                                                                                       C. purpureus delta6-acetylenase/delta6-desaturase SEQ ID
                                                                                                                                                                                                                                                                                                                                                             06-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                       AAB46435 standard;
                                        Example 8; Page 44-46; 69pp; German.
                                                                                                         N-PSDB; AAF25729
                                                                                                                                                          (BADI ) BASF
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99DE-1062409
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                                                                                                                                    Sperling
                                                                       desaturase, useful for of unsaturated fatty acids
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                                                                                                                                     Zaehringer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
                                                                                                                                       C. purpureus delta6-acetylenase/delta6-desaturase SEQ
                                                                                                                                                                            06-APR-2001
                                                                                                                                                                                                                                                AAB46436 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 VPDEELTRM--WSRFMVLNQTWFYFPILSFARLSWCLQSILFVL-PNGQAHKPSGARVPI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 atfhppaawkqlndyyigdl---areepldellkdyrdmraefvreglfksskawfllqt 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity hes 177; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                          sk----dfvraqvittrntkrgwfndwftggldtqiehhlfptmprhnypklapqvealc
                                                                                                                                                                                                                                                                                                                                                                                                                        EEAVDMDFFTKQIITGRDVHPGLFANWFTGGLNYQIEHHLFPSMPRHNFSKIQPAVETLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gliekgtvafhyawfswaafhilpgvakplawmvatelvaglllgfvftlshngkevyne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLVEQLSLAMHWTWYLATMFLFIKDPVNMLVYFLVSQAVCGNLLAIVFSLNHNGMPVISK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   veskrilrvlqyqhymil-----pllfmaryswtfgsllftfnpdlsttk-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGAFLGGVCQGFSSSWWKDKHNTHHAAPNVHGE-----DPDIDTHPLLTWSEHALEMFSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fgylfgncvlgfsvswwrtkhnihhtapnecdegytpldedidtlpiiawsk---eilat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.1%; Score 841.5; DB 22; 39.2%; Pred. No. 4e-78; tive 72; Mismatches 159;
                                                                                                                                                                                                                                                483
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                                                                                                                                                                                                                                                                                                                                       477
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Ceratodon purpureus

WO200075341-A1

Delta6-acetylenase; delta6-desaturase; unsaturated transgenic plant; plant oil; triglyceride; nutritic

nutrition;

animal

feed;

fatty

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YS.
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                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel isolated nucleic acid (I) encoding CC polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase CC activity. The invention also describes (a) amino acid sequences encoded by (I); (b) an expression cassette (EC) containing (I) linked to one or CC more regulatory sequences; (c) a vector containing (I) and EC; (d) CC organisms containing (I), EC or the vectors of (C); (e) preparation of CC unsaturated fatty acids (A) or triglycerides (TG) with increased content of (A) by introducing (I) or EC into an oil-producing organism; (f) CC production of (A) or TG by using (Ia); and (h) (A) and TG produced by CC method (g). (I) are used to produce transgenic plants (or other CC organisms) that produce oils or triglycerides (TG) with increased content CC of unsaturated fatty acids (A) and to isolate related sequences by CC homology screening. (A), or TG containing them, are useful in human CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, CC can be used to suppress expression of (II), resulting in oils with CC increased content of saturated fatty acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 8; Page 49-50; 69pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BADI ) BASF
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189
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nes 177; Conserv
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                                                                                                                                                     VPDEELTRM--WSRFMVLNQTWFYFPILSFARLSWCLQSILFVL-PNGQAHKPSGARVPI 300
                                                                                                                                                                                                                                                     linaalfaasiaticy--dksywaivlsaslmglfvqqcgwlahdflhqqvfenrtansf 228
                                                                                                                                                                                                                                                                       SENLCIMGLSTVIVAKMGQTSTLANVLSAALLGLEWQQCGWLAHDFLHHQVFQDREWGDL
                                                  gliekgtvafhyawfswaafhilpgvakplawmvatelvaglllgfvftlshngkevyne
                                                                                                                                                                                                                                                                                                                                                                                                            TETRAEVLNAEALNEGKKDAEAPFLMIIDNKVYDVREFVPDHPGGSVILTHVGKDGTDVF 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-112150/12.
DB; AAF25730.
                                                                                  SLVEQLSLAMHWTWYLATMFLFIKDPVNMLVYFLVSQAVCGNLLAIVFSLNHNGMPVISK 360
                                                                                                                                                                                                                    FGAFLGGVCQGFSSSWWKDKHNTHHAAPNVHGE-----DPDIDTHPLLTWSEHALEMFSD 243
                                                                                                                                                                                                                                                                                                                                                          DTFHPEAAWETLANFYVGDIDESDRDIKNDDFAAEVRKLRTLFQSLGYYDSSKAYYAFKV 128
                                                                                                                                                                                                                                                                                                                                                                                           tysladv-----ashdrpgdcwmivkekvydisrfaddhpggtvistyfgrdgtdvf 113
                                                                                                                     veskrilrvlqyqhymil-----pllfmaryswtfgsllftfnpdlsttk-----
                                                                                                                                                                                      fgylfgncvlgfsvswwrtkhnihhtapnecdegytpldedidtlpiiawsk---eilat 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                483 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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99DE-1062409
                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.1%; Score 841.5;
39.2%; Pred. No. 4e;;
tive 72; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .5; DB 22;
4e-78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        desaturase, useful of unsaturated fatt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fatty acids
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Query Match
Best Local S
Matches 165
                                                                                                                 produce transgenic plants, especially crop plants, with an increased or decreased delta-8 unsaturated long-chain base content or an altered delta-8 unsaturated long-chain base content or an altered compensate for a delta-8 -unsaturated long-chain base defta-lency, to exclude production of delta-8-unsaturated bases, to increase tolerance or resistance to soil salinity, ion stress or toxicity, drought, wet conditions, cold or frost and/or phytopathogenic microorganisms or later size growth and flowering time. Cells, transgenic organisms or plants containing the DNA sequence can be used to produce sphingolipids and capnoids with unsaturated sphingobases. The sphingolipids or capnoids can be used in cosmetics, pharmaceuticals and foods and as chemical raw materials. This sequence represents a protein which has delta6 fatty acid desaturase activity which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                     introduces a double bond into the sphingobase of the ceramide residue sphingolipids and capnoids. A DNA sequence encoding the sphingolipid desaturase, or a vector containing the DNA sequence, can be used to
                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel sphingolipid desaturase that selectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transgenic plant; crop plant; delta-8-unsaturated long-chain base; tolerance; resistance; soil salinity; ion stress; toxicity; drought; cold; frost; phytopathogenic microorganism; flowering time; cosmetic; pharmaceutical; food; chemical raw material.
                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 16; 62pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heinz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein b5pp with delta6 fatty acid desaturase activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                into sphingolipids and capnoids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New sphingolipid desaturase that selectively introduces double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH
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 al Similarity
165; Conser
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 Conservative
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                33.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schmidt H,
                                                                                                                                                                                                                                                                                                                                                                                                                                              German.
Score 818; DB 21;
Pred. No. 1.2e-75;
6; Mismatches 142
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                                  Length 525;
   32;
 Gaps
   10;
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ARBSULT 1
ARAB4610 1
ID AAB44
XX AAB4
XX AAB4
XX Delt
KW Delt
KW Gatt
XX Belt

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This invention describes a novel preparation of unsaturated fatty acid (I) by introducing into an organism at least one isolated nucleic acid (II) that encodes a polypeptide (III) with Delta6-desaturase activity. Organisms that contain at least with (I), on total fatty acid conten are then selected. (II) is selected from: (a) a 2012 bp sequence (S1), defined in the specification, or its equivalents within the degeneracy
                                                                                                                                                                                                                                          Production of unsaturated fatty acids, useful e.g. in nutrition, cosmetics or pharmaceuticals, in organisms transformed with Physcomitrella patens delta-6-desaturase nucleic acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                  Heinz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUL-1999; 99US-0347531.
30-JUN-2000; 2000DE-1030976.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-JUL-2000; 2000WO-EP06223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agricultural chemical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Delta6-desaturase; unsaturated fatty acid; transgenic; oil; lipid; fatty acid; human nutrition; animal nutrition; cosmetic; pharmaceu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P. patens delta6-desaturase protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB46810 standard;
                                                                                                                                                                                     Claim lc; Page 41-43; 49pp; German.
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                                                                                                                                                   Fatty acid delta-8 desaturase; polyunsaturated;
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Best Local Similarity 33.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Purified protein having double-bond between two
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                                         fsvgqihetmnirrgiitdwffgglnyqiehhlwptlprhnltavsyqveqlcqkhnlpy
                                                            FFTKQIITGRDVHPGLFANWFTGGLNYQIEHHLFPSMPRHNFSKIQPAVETLCKKYNVRY 427
                                                                                                                                          LAMHWTWYLATMELEIKDPVNMLVYELVSQAVCGNLLAIVESLNHNGMPVISKEEAVDMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                   kskrqalsplqlm--eqtydvsawvnfhpggaeiienyqgrdatdafmvmhfqeafdklk 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGKKDAEAPFLMIIDNKVYDVREEVPDHPGGS-VILTHVGKDGTDVFDTFHPEAAWETL- 80
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                                                                                                                                                                                                                                                                                                      lglgvlgyflmvqyqm-----yfigavllgmhyqqmgwlshdichhqtfknrnwnnlvgl 165
                                                                                                                                                                                                                                                                                                                                                                    rmpkinpsfelppqaavneaqedf-----rklreeliatgmfdasplwysykistt 110
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358..362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.6%; Score 631; DB 21; 33.0%; Pred. No. 1.7e-56; tive 76; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         desaturase activity, useful for creating carbons
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VFQDRFWGDLFGAFLGGVCQGFSSSWWKDKHNTHHAAPNVHGEDPDIDTHPL-LTWSEHA

64 80

elkkecptgepeipdikddpikgiddvnmgtfnisekrsaginksftdlrmrvraeglmd 123

SSKAYYAFKVSFNLCIWGLSTVIVAKWGQTSTLANVLSAALLGLFWQQCGWLAHDFLHHQ 178

25 4

Conservative

76;

62;

Gaps

13

KKDAEAPFLMIIDNKVYDVREFV-PDHPGGSVILTHVGKDGTDVFDTFH----PEA-AWET 79

regehepffikidgkwcqiddavlrshpggsaittyknmdattvfhtfhtgskeayqwlt 63 LANFYYGDIDESDRDIKNDDF--------AAEVRK----LRTLFQSLGYYD 118

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RESULT 14
AAY21891
ID AAY218
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Query Match
Best Local S
Matches 154
                                                                                                                                               genes can be used in gene therapy as a preventative treatment, e.g. in patients suffering from high levels of coblesterol or other conditions where administration of polyunsaturated fatty acids may have beneficial disease preventative effects. The polyunsaturated fatty acids can be used in foodstuffs or dietary supplements. The Delta 5-fatty acid desaturases
                                                                                                                  in foodstuffs or dietary supplements. The Delta 5-fatty acid desaturases can also be used for the synthesis of prostaglandins or modulation of the synthesis. The products can also be used for detection and diagnosis. The
                                                                         Sequence
                                                                                                                                                                                                                          The invention provides delta 5-fatty acid desaturases obtained from Mortierella alpina and Caenorhabditis elegans. The Delta 5-fatty acid desaturases catalyze the production of polyunsaturated fatty acids, e the conversion of dihomogamma linolenic acid to arachidonic acid. The
                                                                                                                                                                                                                                                                                                      Claim 18;
                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAX86961.
                                                                                                                                                                                                                                                                                                                                                                                                                        Michaelson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dietary supplement; prostaglandin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Delta 5-fatty acid desaturase; dihomogamma linolenic arachidonic acid; cholesterol; polyunsaturated fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C. elegans delta 5-fatty acid desaturase
                                                                                                      present sequence represents the C. elegans
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-444067/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                New isolated delta5-fatty acid desaturase enzymes useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYBR-) UNIV BRISTOL
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97GB-0027256.
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               25.5%;
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 Score 629; DB 20;
Pred. No. 3.1e-56;
6; Mismatches 175;
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polyunsaturated fatty acid;
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foodstuff;
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                                                                                                 This is the Caenorhabditis elegans fatty acid delta-5 desaturase. The CDNA sequence is useful for recombinant production of the enzyme and for generating transformed host cells and transgenic plants. The desaturase can be used for creating a double-bond between two carbons. In particular, the enzyme is useful for producing polyunsaturated fatty acids and for generating enzyme-specific antibodies useful for identifying desaturases. Oil-seed plants may be engineered to incorporate the enzyme, so that the plants produce seed oil rich in fatty acids. The fatty acids could be incorporated usefully into infant formula, foods of all kinds, dietary supplements, nutriceutical and pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C. elegans fatty acid delta-5-desaturase
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                                                                                                                                                                                                                                                Claim 3; Fig 6A; 74pp;
                                                                                                                                                                                                                                                                        Purified protein having double-bond between two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                   desaturase activity, useful for creating
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76;
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6; Mismatches 175;
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lntvmplvkefaaanglpymvddyftgfwleiegfrnianvaakltk
                              FSKIQPAVETLCKKYNVRYHTTGMIEGTAEVFSRLNEVSKAASKMGK 455
                                                            tfnhysvekfalssnimsnyaclqimttrnmrpgrfidwlwgglnyqiehhlfptmprhn
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Qy Db

61 GKDGTDVFDTFHPEAAWETLANFYVGDIDESDRDIKNDDFAAEVRKLRTLFQSLGYYDSS 120

45	44	43	42	41	40	39	38	37	36	35	34	<u>ω</u>	32	31	30	29	28	27	26	25	24	23	22	21	20
212	227	228	280.5	297.5	306	337.5	384.5	386	416	422.5	431	437.5	439	445.5	447.5	460	460.5	462.5	478.5	488.5	492	497	497.5	502	506
8.6	9.2	9.2	11.4	12.1	12.4	13.7	15.6	15.7	16.9	17.1	17.5	17.7	17.8	18.1	18.2	18.7	18.7	18.8	19.4	19.8	20.0	20.2	20.2	20.4	20.5
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060426 homo sapien	Q54795 spirulina p	Q9n9b5 leishmania	074212 mortierella	Q9y1w0 dictyosteli	096099 dictyosteli	Q9y3x4 homo sapien	Q9f2m3 streptomyce	Q9h3g3 homo sapien	Q9dex6 cyprinus ca	īΩ	Q9hdg8 mucor roux1	Q9fc35 streptomyce	Q9dex7 brachydanio	Q9z122 rattus norv	Q9z0r9 mus musculu	095864 homo sapien	Q9fr82 borago off1	Q9jje7 mus musculu	Q9y5q0 homo sapien	Q9ztz9 arabidopsis	Q9ztu8 triticum ae	Q9zty9 ricinus com		Q9zrp8 brassica na	Usepv4 raccus norv

ALIGNMENTS

	I MAAAPSYKTETKAEVLNAEALNEGKKOAEAPELMILINKYTDYKEFYPDHYGGSYLITHY 60 	да Су
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	Heille. SEQUENCE 457 AA; 51837 MW; D90169E86911450A CRC64;	SQ
	ITE;	DR
	Ptam; PFUU173; heme_1; 1. PROSITE; PSU0191; CYTOCHROME_B5_1; UNKNOWN_1.	DR DR
	InterPro; IPR001199;	DR
	HSSP; P04166; 1B5M.	DR DR
		RL
	cerevisiae.";	RT
	and recombinant production of gamma-linolenic acid in Saccharomyces	RJ :
	"Cloning of deltal2- and delta6-desaturases from Mortierella alpina	RAS
	Huang Y.S., Chaudhary S., Thurmond J.M., Bobik E.G. Jr., Yuan L.,	RA
	MEDLINE-99406036; PubMed-10478922;	RX
	STRAIN-ATCC32221;	RC
	SEQUENCE FROM N.A.	RP
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	Mortierella.	റ്റ
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	DELTA-6 FATTY ACID DESATURASE.	5 5
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Pfam; PF00173; heme_1; 1.
PROSITE; PS00191; CYTOCHROME_B5_1; UNKNOWN_1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20035749; PubMed=10570972; Sakuradani E., Kobayashi M., Shimizu S.; "Delta 6-Fatty acid desaturase from an ara Mortierella fungus. Gene cloning and its fungus, Aspergillus."; Gene 238:445-453(1999).
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Eukaryota; Fungi; Z
Mortierella
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DELTA-6 FATTY ACID DESATURASE.
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                                             GKDGTDVFDTFHPEAAWETLANFYVGDIDESDRDIKNDDFAAEVRKLRTLFQSLGYYDSS 120
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Q9HEY4;
01-MAR-2001
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EMBL; AF306634; AAG38104.1; -. 868E7EB21172D5AF CRC64;
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01-MAR-2001 (TrEMBLrel. 16, L
DELTA6-FATTY ACID DESAFURASE.
Mortierella isabellina.
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Ming-Chun L., Li L.,
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01-MAR-2001 (TrEMBLrel. 16, La
01-MAR-2001 (TrEMBLrel. 16, La
DELTA 6-FATTY ACID DESATURASE.
MORTLIERELLA alpina.
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Xing L., Li M., Liu L., Hu G., Zhang L.;
"Expression of Mortierella alpina delta 6-fatty acid des
in Saccharomyce cerevisiae.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF307940; AAAG45092.1;
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SEQUENCE 457 AA: 51885 MW; 4B0AC0DD15D19DA1 CRC64;
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Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-OCT-2001 (TrEMBLrel. 16, Last annotation update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DELTA 6-FATTY ACID DESATURASE.
Ceratodon purpureus (Moss).
Eukaryota; Viridiplantae; Embryophyta; Bryophyta;
Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
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01-MAR-2001 (TrEMBLrel. 16, Last annotation
DELTA 6-FATTY ACID DESATURASE (FRAGMENT).
Mortierella alpina.
Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierella....
SEQUENCE FROM N.A.
STRALN=WT3: TISSUE=PROTONEMATA;
MEDLINE=20307617; PubMed=10848999;
Sperling P., Lee M., Girke T., Zae
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Xing L., Li M., Liu L., Hu G., Zhang L.;
"Cloning and sequence analysis of the conserved region fatty acid desaturase gene from Mortierella alpina.";
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"Cloning and sequence analysis of the conserved region (
fatty acid desaturase gene from Mortierella alpina.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2001 (TrEMBLrel. 16,
DELTA 6-FATTY ACETYLENASE.
                                                                                                                                                                                                                                                                                                                                                                 Ceratodon purpureus (Moss).
Eukaryota; Viridiplantae; Embryophyta; Bryophyta;
Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-WT3; TISSUE-PROTONEMATA;
MEDLINE-20307617; Pubmed-10848999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eur. J. Blochem. 267:3801-3811(2
EMBL; AJ250735; CAB94993.1; -.
InterPro; IPR001199; -
Pfam; PF00173; heme_1; 1.
PROSITE; PS50255; CYTOCHROME_B5_
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                                                 Eur. J. Biochem. 267:3801-3811(2000).
EMBL; AJ250734; CAB94992.1; -.
InterPro: IPR001199; -.
                                                                                                                                                          Sperling P., Lee M., Girke T., Zaehringer U., Stymne S., I "A bifunctional delta 6-fatty acyl acetylenase/desaturase moss Ceratodon purpureus. A new member of the cytochrome I
Pfam; PF00173; heme_1; 1.
PROSITE; PS50255; CYTOCHROME_B5_2;
                                                                                                                                                        moss Ceratodon purpureus. A
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                                                                                                                                 superfamily.";
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15, Last sequence update;
16, Last annotation updat
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Pred. No. 1e-71;
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                                                      STRAIN-HEDW. B. S. G.;

MEDLINE-98416756; PubMed-9744093;

Girke T., Schmidt H., Zaehringer U., Reski R., Hu
"Identification of a novel delta 6-acyl-group des
"gene disruption in Physocmitrella patens.";

plant J. 15:39-48(1998).

-I- SIMILARITY: TO CYTOCHROME B5 DOMAIN.

EMBL; AJ222981; CAA11033.1; -.

EMBL; AJ222980; CAA11032.1; -.

HSSP; P04166; 1B5M.
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Best Local Similarity
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                                                                                                                                                                                                                                                                Q9ZNW2;
Q9ZNW2;
Q1-MAY-1999
Q1-MAY-1999
Q1-MAR-2001
Heme.
SEQUENCE
                                                                                                                                                                                                     Physcomitrella patens (Moss).
Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;
Funariidae; Funariales; Funariaceae; Physcomitrella.
                                                                                                                                                                                                                                             DES6.
                                                                                                                                                                                              NCBI_TaxID=3218;
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                      PROSITE;
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                                            InterPro; IPR001199; -.
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Query Match

33

Score 818;

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10;

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Best

38.8%;

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                                                                                                                                                                                                                                                                                                                                                                                 "Isolation and characterisation of a delta5-fatty Ceanorhabditis elegans."; Arch. Biochem. Biophys. 362:175-182(1999).
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                                                                                                                                                    SEQUENCE FROM N.A.
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MEDLINE=99117288; PubMed=9917342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
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Caenorhabditis elegans.
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01-NOV-1999
                                            SEQUENCE FROM N.A. MEDLINE=99069613;
                                                                                                                   Submitted
                                                                                                                                                                                                     Caenorhabditis elegans.";
FEBS Lett. 439:215-218(1998)
                                                                                                                                                                                                                                             "Functional identification of a fatty acid
                                                                                                                                                                                                                                                                                          MEDLINE-99059458; PubMed-9845325; Michaelson L.V., Napier J.A., Lew
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Watts J.L., Browse J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
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Last sequence update)
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Best Local S
Matches 154
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01-MAY-2000
01-MAY-2000
01-MAR-2001
            InterPro;
PROSITE;
                               "The Delta8-desaturase of Euglena gracilis: an synthesis of 20-carbon polyunsaturated fatty ac Arch. Biochem. Biophys. 365:307-316(1999).
EMBL: AF139720; AAD45877.1;
                                                                                                                                    Euglena gracilis.
Eukaryota; Euglenozoa;
Eukaryota; Oglenozoa;
NCBI_TaxID=3039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     investigating biology.";
Science 282:2012-2018(1998).
EMBL; AF114440; AAD13294.1; -.
EMBL; AF078796; AAC95143.1; -.
EMBL; 281122; CAB61031.1; -.
                                                                                                       STRAIN-Z
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SEQUENCE
                                                                              Wallis J.G., Browse J.;
                                                                                          MEDLINE=99262077; PubMed=10328826;
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2.2e-49;
nes 175;
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                                                                                                                                                                                                update)
                                                        an alternate acids.";
                                                                                                                                                   Euglena
 CRC64;
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                                                                   pathway
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Query Match Best Local Similarity

25.3%;

Score Pred.

624.5; DB 10; No. 5.2e-49;

Length

12

71

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RESULT
O23321
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Best Local Similarity
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01-NOV-1996
01-MAY-2000
01-MAR-2001
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Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Swinburne J., Ainscough
Submitted (MAR-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W08D2.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q23221
                                                                                                                                                                                                                                                                                                                     Science
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                 InterPro; IPR000566; -.
                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                              investigating biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                     Genome sequence of the nematode C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              388
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34 MIIDNK-VYDVREFVPDHPGGSVILTHVGKDGTDVFDTFHPEAAW---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LCIWGLSTVIVAKWGQTSTLANVLSAALLGLFWQQCGWLAHDFLHHQVFQDRFWGDLFGA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSKRQALSPLØLM--EQTYDVVNF---HPGGAEIIENYQGRDATDAFWVMHFQEAFDKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGKKDAEAPF,LMIIDNKYYDVREFVPDHPGGS-VILTHVGKDGTDVFDTFHPEAAWETL-: |: |: | | | | | | | : |:: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGLGYLGYFLMYQYQM-----YFIGAVLLGMHYQQMGWLSHDICHHQTFKNRNWNNLVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNPLPHEGLVILLRYLAVFARMAEKQPA----GKA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTTGMIEGTA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --SRKLIQFQQYYFLVICILLRFIWCFQCVLTVRSLKDRDNQFYRSQYKK-----EAIG
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                                                                                                                                                                                                                                                                                                ce 282:2012-2018(1998).
270271; CAA94233.2; -.
                                                                                                                                                                                  PS50255; CYTOCHROME_B5_2; 1.
PS00213; LIPOCALIN; UNKNOWN_1.
443 AA; 51772 MW; 9513D611ECB99A06 CRC64;
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                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nematoda; Chromadorea; cinae; Caenorhabditis.
                                                                                          22.7%;
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Last annotation updat
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5.9e-43;
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                                                                        187;
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                                                                                                               Length 443;
                                                                        Indels
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   Matches
                Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=97268723; PubMed=9108131;
Sayanova O., Smith M.A., Lapinskas P., Stobart A.K., Dodson, Christie W.W., Shewry P.R., Napier J.A.;
"Expression of a borage desaturase cDNA containing an N-terminal cytochrome b5 domain results in the accumulation of high levels delta6-desaturated fatty acids in transgenic tobacco.";
delta6-desaturated fatty acids in transgenic tobacco.";
matl. Acad. Sci. U.S.A. 94:4211-4216(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       061388 PRELIMINARY; 1
061388; 01-806-1998 (TrEMBLrel. 07, Cre
01-AUG-1998 (TrEMBLrel. 07, Las
01-MAR-2001 (TrEMBLrel. 16, Las
DELTA6-FATTY-ACID-DESATURASE.
                                                              InterPro; IPROUVO-;
InterPro; IPRO01199; -.
InterPro; IPRO01199; -.
PROSITE; PS00255; CYTOCHROME_B5_2;
PROSITE; PS00213; LIPOCALIN; UNKNOF
PROSITE; PS00213; LIPOCALIN; UNKNOF
                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=98149727; PubMed=9480865;
MEDLINE=98149727; PubMed=9480865;
Napier J.A., Hey S.J., Lacey D.J., Shewry P.R.;
"Identification of a Caenorhabditis elegans Delta6-fatty-acid-"Identification of a Caenorhabditis elegans Delta6-fatty-acid-"
"Identification of a Caenorhabditis elegans Delta6-fatty-acid-"
"Identification of a Caenorhabditis elegans Delta6-fatty-acid-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
                                                                                                                                               desaturase by heterologous expression Biochem. J. 330:0-0(0). EMBL, AF031477; AAC15586.1; -. InterPro; IPR000566; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTRMWSRF-----MVLNQTWFYFPILSFARLSWCLQSILFVLPNGQAHKPSGARVPISL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETLANFYYGDIDESDRDIKNDDFA-AEVRKLRTLFQSL------GYYDSSKAYYAFKVS
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   143;
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nematoda; Chromadorea; rinae; Caenorhabditis.
                22.6%;
32.1%;
   64;
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Score 557; DB
Pred. No. 9.1e
54; Mismatches
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                                                                             UNKNOWN_1.
; 9513CA7C5A7E9A06
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               DB 5;
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 187;
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                                Length 443;
                                                                                  CRC64;
   Indels
                                                                                                                                                                                                   cerevisiae.";
   52;
 Gaps
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                                                                     Query Match
Best Local Similarity
                                                         Matches
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CYTOCHROME B5 CONTAINING FUSION PROTEIN.
Helianthus annuus (Common sunflower)
Elkaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae;
euasterids II; Asterales; Asteraceae; Asteroideae; Heliantheae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q43469;
Q43469;
                                                                                                                              Heme.
SEQUENCE
                                                                                                                                                        Interpro; IPR001199; -.
Pfam; PF00173; heme_1; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
                                                                                                                                                                                                 Eur. J. Biochem. 232:798-805(1995)
-!- SIMILARITY: TO CYTOCHROME B5 D
EMBL; X87143; CAA60621.1; -.
HSSP: P00171; IWDB.
Mendel: 8443; Helan; 2419; 8443.
                                                                                                                                                                                                                                                                                                    STRALN-CV INBRED LINE HA89, SF163 /91;
TISSUE-COTYLEDONS OF DEVELOPING SUNFLOWER
MEDLINE-96028121; PubMed-7588718;
Sperling P., Schmidt H., Heinz E.;
                                                                                                                                                                                                                                                                           desaturases.";
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           Helianthus
                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4232;
                                                                                                                                                                                                                                                                                        A cytochrome-b5-containing fusion
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               APSVRTETRAEVLNAEALNEGKKDAEAPFLMIIDN-------KVYDVREFVPDHPGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKVDGKWLYLSEELVKKHPGGAVIEQYRNSDATHIFHAFHEGSSQAYKQLDLLKKHGEHD
 SPSI----
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                                                                                                                              458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                       Conservative
-EVLNSIA--DGKKYITSKELKKHNNPNDLWISILGKVYNVTEWAKEHPGG
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                                                                                                                              52231 MW;
                                                                     21.7%;
                                                    Score 534.5; DB 10
Pred. No. 1.1e-40;
1; Mismatches 201;
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Q9NYX1;
Q1-OCT-2000
Q1-OCT-2000
Q1-MAR-2001
                                                                                                                                                                                                                                                   Pfam; PF00173; heme_1; 1.
PRINTS; PR00363; CYTOCHROMEB5.
PROSITE; PS50255; CYTOCHROME_B5
                                                                                                                                                                                                                                                                                              -1- SIMILARITY: TO CYTOCHROME B5 DOMAIN..
EMBL; AF226273; AAF70457.1; -.
InterPro; IPR001199; -.
                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20233676; PubMed-10769175;
Leonard A.E., Kelder B., Bobik E.G., Chuang
Thurmond J.M., Kroeger P.E., Kopchick J.J.,
"CDNA cloning and characterization of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVILTHY-GKDGTDYFDTFHPEAAWETLANFYYGDIDESDRDIKNDDFAAEVRKLRTLFQ 112
                                                         GKDGTDVFDTFHPEAAW--ETLANFYVGDI----DESDRDIKNDDFAAEVRKLRTLFQSLG
                                                                                                                  AAAPSVRTFTRAEVLNAEALNEGKKDAEAPFLMIIDNKVYDVREFVPDHPGGSVILTH-V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RCHLRSISPICRELCKKYNLPYVSLSFYDANVTTLKTLRTAALQA 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IQFTLNHFSGDVYVGPPKGD-NWFEKQTRGTIDIACSSWMDWFFGGLQFQLEHHLFPRLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IVFSLNHNGMPVISKEEAVDMDFFTKQIITGRDVHPGLFANWFTGGLNYQIEHHLFPSMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GHDAGHYQMMATRGWNKFAGIFIGNCITGISIAWWKWTHNAHHIACNSLDYDPDLQHLPM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLGYYDSSKAYYAFKVSFNLCIWG--LSTVIVAKWGQTSTLANVLSAALLGLFWQQCGWL 170
YYDSSKAYYAFKVSFNLCIWGLSTVIVAKWGQTSTLANVLSAALLGLFWQQCGWLAHDFL
                             GQDATDPFVAFHINKGLVKKYMNSLLIGELSPEQPSFEPTKNKELTDEFRELRATVERMG
                                                                                      AQGPTPRYFTWDEVAQRSGCEER-----WLVIDRKVYNISEFTRRHPGGSRVISHYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHNFSKIQPAVETLCKKYNVRYHTTGMIEGTAEVFSRLNEVSKAA 450
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0 (TrEMBLrel. 15, Las
1 (TrEMBLrel. 16, Las
TTY ACID DESATURASE.
                                                                                                                                                                                                                          444 AA;
                                                                                                                                                 Conservative
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                                                                                                                                                                                                                          51968 MW;
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30.1%;
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Last annotation updat
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                                                                                                                                                              Score 524.5;
Pred. No. 8.8
                                                                                                                                                                                                                          40F13C72AEAEBE3D CRC64;
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                                                                                                                                                 Mismatches
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                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                       L.-T., Parker-Barnes
Huang Y.-S., Mukerji
delta-5 desaturase
                                                                                                                                                 196;
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                                                                                                                                                                            Length 444;
                                                                                                                                                 Indels
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RESULT
060427
                                                                           Marquardt A., Stohr H., White K., Weber B.H.F.;
RT "cDNA cloning, genomic structure, and chromosomal lc
three members of the human fatty acid desaturase fam
'L Genomics 66:175-183(2000).
'C '-' SIMILARITY: TO CYTCCHROME B5 DOMAIN.

R EMBL; AC004770; AAC23397.1; --
R EMBL; AL512760; CAC21679.1; --
R EMBL; AL512760; CAC21679.1; --
HSSP; P04166; 1B5M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
BC269730_2 (HYPOTHETICAL 52.0 KDA PROTEIN) (FATTY ACID DESATURASE 1).
                                           InterPro; IPR001199; -.
Pfam; PF00173; heme_1; 1.
PRINTS; PR00363; CYTOCHROMEB5
                                                                                                                                                                                                                                                                         TISSUE-MELANOMA (MEWO CELL LINE);
Blum H., Bauersachs S., Mewes H.W., Weil B., W
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                      Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKFZP762M2311 OR FADS1.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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 SEQUENCE
                              PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTQMNHIPMHI---DHDRNMDWVSTQLLATCNVHKSAFNDWFSGHLNFQIEHHLFPTMPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LMKANHVFFLLYLLHILLLDGAAWLTLWVFG-TSFLPFLLCAVLLSAVQAQAGWLQHDFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HNFSKIQPAVETLCKKYNVRYHTTGMIEGTAEVFSRLNE 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HALEMFSDVPDEELTRMWSRFMVLNQTWFYF-----PILSFARLSWCLQSILFVLPNGQA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VFSLNHNGMPVISKEEAVDMDFFTKQIITGRDVHPGLFANWFTGGLNYQIEHHLFPSMPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------IQRKKWVDLAWMITFYVRFFLTYV--PLLGLKAFLGLFFIVRFLESNWFVW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLSVFSTSKWNHLLHHFVIGHLKGAPASWWNHMHFQHHAKPNCFRKDPDINMHPFF----
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                              PS50255;
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                            CYTOCHROME_B5_2;
 51964 MW;
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CC3C28D82AA49BF2 CRC64;
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Best Local Similarity
 394
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                                                     YYDSSKAYYAFKVSFNLCIWGLSTVIVAKWGQTSTLANVLSAALLGLFWQQCGWLAHDFL 175
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                                                                                          VFSLNHNGMPVISKEEAVDMDFFTKQIITGRDVHPGLFANWFTGGLNYQIEHHLFPSMPR 406
                                                                                                                                                                                    FALGKILSV---ELGKQKKKYMPYNHQHKYFFLIGPPALLPLYFQWYI--FYFV-----
                                                                                                                                                                                                     HALEMFSDVPDEELTRMWSRFMVLNQTWFYF-----PILSFARLSWCLQSILFVLPNGQA
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                                                                                                                                                                                                                                                                                                                                                                                                    GKDGTDVFDTFHPEAAW--ETLANFYVGDI----DESDRDIKNDDFAAEVRKLRTLFQSLG
HNYHKVAPLVQSLCAKHGIEYQSKPLLSAFADIIHSLKE
                              HNFSKIQPAVETLCKKYNVRYHTTGMIEGTAEVFSRLNE 445
                                                                                                                                                    HKPSGARVPISLVEQLSLAMHWTWYLATMFLFIKDPV----NMLVYFLVSQAVCGNLLAI
                                                                                                                                                                                                                                             HLSVFSTSKWNHLLHHFVIGHLKGAPASWWNHMHFQHHAKPNCFRKDPDINMHPFF----
                                                                                                                                                                                                                                                                                                                                                                                                                                AQGPTPRYFTWDEVAQRSGCEER------WLVIDRKVYNISEFTRRHPGGSRVISHYA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                        IQRKKWVDLAWMITFYVRFFLTYV--PLLGLKAFLGLFFIVRFLESNWFVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.2%; 30.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 523.5; DB 4;
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Search completed: August 9, 2001, 20:36:14 Job time: 713 sec

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Minimum DB
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Listing first 45 summaries
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Perfect score:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Query Match 8.5 Best Local Similarity 25.7 Matches 83; Conservative

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CYS5_TOBAC
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P49099;
BINDING
BINDING
TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Napier J.A., Smith M.A., Stobart A.K., Shewry P.R.;

"Isolation of a cDNA encoding a cytochrome b5 specifically expressed in developing tobacco seeds.";

Planta 197:200-202(1995).

-!- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND OXYGENASES. MAY PLAY A KEY ROLE IN THE MODIFICATION BY DESATURATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH INTELLIBRATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH INTELLIBRATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH INTELLIBRATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH INTELLIBRATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH INTELLIBRATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH INTELLIBRATE ACIDS IN THE MEMBRANE SYNTHESIS AND IN THE
                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-series.
                PROSITE; PS00191; CYTOCHROME_B5_1; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
Electron transport; Transmembrane; Heme;
BINDING 40 40 HEME LIGAND
BINDING 64 HEME LIGAND
TRANSMEM 107 127 POTENTIAL.
                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-FEB-1996 (Rel. 33, Last seq
01-OCT-2000 (Rel. 40, Last ann
CYTOCHROME B5, SEED ISOFORM.
                                                                                                                    PRINTS; PR00363; CYTOCHROMEB5
                                                                                                                                        Pfam;
                                                                                                                                                                       EMBL; X80008; CAA56318.1; HSSP; P00171; LWDB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nicotiana tabacum (Common tobacco)
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                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULM (BY SIMILARITY) TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING SEED SIMILARITY; BELONGS TO THE CYTOCHROME B5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVELOPMENTALLY REGULATED PRODUCTION OF LARGE AMOUNTS
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                                                                                                                                      PF00173; heme_1;
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Pred. No. 3
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   A36CCA081A72ECBC
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eudicots; Asteridae; euasterids
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.2e-06;
                                Microsome; Multigene family.
(BY SIMILARITY).
(BY SIMILARITY).
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Query Match 6.3 Best Local Similarity 45.3 Matches 39; Conservative

6.2%;

Score 153; Pred. No. 7

DB 1; .le-06;

Length 135 Inde1s

10;

Gaps

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Mismatches

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01-FEB-1996 (R
01-OCT-2000 (R
CYTOCHROME B5.
                                                                                                                                  TRANSMEM
CONFLICT
CONFLICT
                                                                                                                                                                                                              BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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Solanales; Solanaceae; Nicotiana
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EMBL; X68140; CAA48240.1;
HSSP; P04166; 1B5M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94325476; PubMed=8049375;
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                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001199;
     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nt Mol. Biol. 25:527-537
FUNCTION: CYTOCHROME B5
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                                                                                                                                                                                                                                                                 transport;
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                                                                                                                                                             ; Transmembrane; Heme; Microsome; Multigene
40 HEME LIGAND (BY SIMILARITY).
64 HEME LIGAND (BY SIMILARITY).
127 POTENTIAL.
11 LA -> EF (IN CAA48240).
6.1%;
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  150; DB 1;
No. 1.3e-05;
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RESULT 5
CY52_ARATH
ID CY52_ARATH
AC 048845;
DT 01-0CT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K. Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J. Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatic
the European Bioinformatics Institute. Thei
use by non-profit institutions as long a
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                                BINDING
                                                                                                                                                     EMBL; AC003974; AAC04491.1; -.
HSSP; P04166; 1B5M.
Mendel; 27943; Arath;1218;27943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CV. COLUMBIA; MEDLINE-20083487; PubMed-10617197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROBABLE CYTOCHROME B5 ISOFORM AT2G32720 OR F24L7.14.
                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brassicales;
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                                                               Electron
                                                                            PROSITE; PS001
PROSITE; PS502
                                                                                                           Pfam; PF00173; heme_1; 1. PRINTS; PR00363; CYTOCHROMEB5
                                                                                                                                                                                                                                                                                                                                                                             -
                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           thaliana."
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                                                                                                                                           [nterPro;
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                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (B SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                            OXYGENASES (BY SIMILARITY).
SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: CYTOCHROME B5 IS A MEMBRANE FUNCTION AS AN ELECTRON CARRIER FOR SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37;
                              transport;
                                                                            PS00191; CYTOCHROME_B5_1; 1. PS50255; CYTOCHROME_B5_2; 1.
                                                                                                                                           IPR001199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 40,
(Rel. 40,
(Rel. 40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brassicaceae; Arabidopsis
   Α
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t; Transmembrane; Heme; M
40 HEME LIGAND (
64 HEME LIGAND (
127 POTENTIAL.
127 POTENTIAL.
; 15016 MW; B405F5430F5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
15 ISOFORM 2.
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   B405F5430F5716C1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134
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                                                                                                                                                                                                                                                                There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                           NE BOUND HEMOPROTEIN WHICH SEVERAL MEMBRANE BOUND
                              Microsome; Multigene (BY SIMILARITY). (BY SIMILARITY).
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   CRC64;
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Query Match Best Local S Matches 29

29; Conserv

Conservative

12;

Score 143; DB 1; Pred. No. 4.7e-05 2; Mismatches 1

15;

2

Gaps

N

Length 134;

50.0%;

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34 MIIDNKVYDVREFVPDHPGG-SVILTHVGKDGTDVF-DTFHPEAAWETLANFYVGDID

89

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CYB5_BA
AC P40334
AC P4034
AC P4034
AC P4034
DT 01-FEB
DT 01-FEB
DT 01-FEB
DT 01-FEB
DT 01-FEB
DT 01-FEB
CYTOCH
GN CYB5.

OS Brassi
OC Eukary
OC Magnol
RC STRAIN
RA KEARNS
RA KEARNS
RA FT "Nucle
RT "Nucle
R
RESULT 7
CYB5_ORYSA
LD CYB5_O
AC P49100
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Best Local
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CYB5_ORYSA
P49100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00173; heme_1; 1.
PRINTS; PR00363; CYTOCHROMEB5.
PROSITE; PS00191; CYTOCHROME_B5_1; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
Electron transport; Transmembrane; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M87514; AAA32990.1; HSSP; P00171; 3B5C. InterPro; IPR001199; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Brassica oleracea L.).";
Plant Physiol. 99:1254-1257(1992).
-!- FUNCTION: CYTOCHROME B5 IS A M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last seq
01-OCT-2000 (Rel. 40, Last ann
CYTOCHROME B5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYB5_BRAOL P40934;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brassica oleracea (Cauliflower).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kearns E.V., Keck P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence of cDNA for cytochrome b5
                                                                                                                                                          64
                                                                                                                                                                                                                                                                                     24
                                                                                                                                                                                                          72
                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way lifted and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY). SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
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                                                                                                                                                          HSDTARDMMEKYYIGEIDSS
                                                                                                                                                                                                          HPEAAWETLANFYVGDIDES 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVINGKVYNVTKFLEDHPGGDDVLLSSTGKDATDDFEDVGHSESAREMMEQYYVGEID
                                                                                                                                                                                                                                                             KVLGFEEVSQHNKTKDC--WLIISGKVYDVTPFMDDHPGGDEVLLSSTGKDATNDFEDVG
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32; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAULIFLORA;
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                                                                                                                                                                                                                                                                                                                                                                   Conservative
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64
127
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15062 MW;
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                                                                                                                                                                                                                                                                                                                                                                                           5.8%;
40.0%;
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                                                                                                                                                          83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
K ~> N.
                                                                                                                                                                                                                                                                                                                                                                Score 143; DB 1;
Pred. No. 4.7e-05;
6; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEME LIGAND
                             PRT;
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(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 134;
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MBL outstation -
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RESULT 8
CY51_ARATH STANDARD; PRT; 134
ID CY342; O9SB05;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence upda
DT 01-OCT-2000 (Rel. 40, Last annotation up
DE CYTOCHROME B5 ISOFORM 1.
OS Arabidopsis thaliana (Mouse-ear cress)
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01-FEB-1996 (Rel. 3
01-OCT-2000 (Rel. 4
CYTOCHROME B5.
                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith M.A., Stobart A.K., Shewry P.R., Napier J.
"Tobacco cytochrome b5: cDNA isolation, expressi
vitro protein targeting."
plant Mol. Biol. 25:527-537(1994).
-i- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND
FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL
                          Eukaryota; Viridiplantae; Embryophyta; Magnoliophyta; eudicotyledons; core eu Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (Rice).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Electron transport;
BINDING 41
BINDING 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001199; -.
Pfam; PF00173; heme_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X75670; CAA53366.1;
HSSP; P00171; 3B5C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00363; CYTOCHROMEB5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4530;
                                                                                                                                                                                                                                        59
                                                                                                                                                                                                                                                                   67
                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY). SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00191; CYTOCHROME_B5_1; 1.
PSS0255; CYTOCHROME_B5_2; 1.
transport; Transmembrane; Heme; Microsome.
41 41 HEME LIGAND (BY SIMILARITY).
65 65 HEME LIGAND (BY SIMILARITY).
108 128 POTENTIAL.
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137 AA;
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No. 0.0001;
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dicots; Rosidae; eurosids II;
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Best Local :
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20-mAR-1987 (Rel. 04, Created)
01-OCT-2000 (Rel. 40, Last sequence up
01-OCT-2000 (Rel. 40, Last annotation
CYTOCHROME B5 OUTER MITOCHONDRIAL MEME
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                                                                   Eukaryota;
Mammalia; E
                                                                                                                                                                                                                                                                           CYM5_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00173; heme_1; 1. PRINTS; PR00363; CYTOCHROMEB5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
       SEQUENCE FROM N.A
                                                                                                                Rattus norvegicus (Rat).
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mitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
OXYGENASES (BY SIMILARITY).
SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (B' SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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PS50255; CYTOCHROME_B5_2; 1.
transport; Transmembrane; Heme;
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HEME LIGAND
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HEME LIGAND
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                                                                   Eutheria;
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Rodentia;
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9CC01C60F7C873FD CRC64;
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Sciurognathi;
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                                                                                         Vertebrata;
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es 27;
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Best Local
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SEQUENCE
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PROSITE; PS00191; CYTOCHROME_B5_1;
PROSITE; PS50255; CYTOCHROME_B5_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochemistry 37:1485-1494(1998).
-I- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=83182449; PubMed=6840088;
Lederer F., Ghrir R., Guiard B., Cortial S., Ito A.;
"Two homologous cytochromes b5 in a single cell.";
Eur. J. Biochem. 132:95-102(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Electron transport, Heme; 3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97128656; PubMed-8973214;
Rodriguez-Maranon M.J., Qiu F., Stark R
Foundling S.I., Rodriguez V., Schilling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kuroda R., Ikenoue T., Honsho M., Tujimoto S., Miroma J., Ito A. "Charged amino acids at the carboxy-terminal portions determine intracellular locations of two isoforms of cytochrome b5."; Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
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64 GTDVF-DTFHPEAAWETLANFYVGDIDESDRDIKNDDFAAEVRKLRTLFQSLGYYDSSKA 122
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SUBCELLULAR LOCATION: MITOCHONDRIAL
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1AWP; 18-NOV-98.
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46; Conser
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HEME LIGAND (BY SIMILARITY).
N -> D (IN REF. 2).
1CA90DD3C81C412E CRC64;
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                    InterPro; IPRO01199; ...
Pfam; PF00173; heme_1; 1.
PRINTS; PR00363; CYTOCHROMEB5.
PROSITE; PS00191; CYTOCHROME_B5_1; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
BINDING
             Electron
                                                                                                   EMBL; L22494; AAA67468.1; -.
EMBL; Z69382; CAA93396.1; -.
EMBL; Z71387; CAA95990.1; -.
EMBL; S47919; S47919.
                                                                                                                                                                                                                between
                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae reveals an unusually overlapping open reading frames."; Yeast 13:261-266(1997).
                                                                                                                                                                                                                                                                                                                                                                   de Antoni A., D Angelo M., Dal Pero F., Sartorello F., Pallavicini A., Lanfranchi G., Valle G.; "The DNA sequence of cosmid 14-13b from chromosome XIV Saccharomyces cerevisiae reveals an unusually high numb
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 142:123-127(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Truan G., Epinat J.-C., Rougeulle C., Cullin C., Pompon D.; "Cloning and characterization of a yeast cytochrome b5-encoding which suppresses ketoconazole hypersensitivity in a NADPH-P-450 reductase-deficient strain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomycetales;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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01-OCT-2000
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01-FEB-1995
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                                                                                                                                                                                                                                           ZYMOSTEROL.

SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).

SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
                                                                                                                                                                                                                                                                                        FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND OXYGENASES. IT PLAYS A ROLE IN FATTY-ACID DESATURATION AND IS INVOLVED IN SEVERAL STEPS OF THE STEROL BIOSYNTHESIS PATHWAY, PARTICULARLY IN THE 4-DEMETHYLATION OF THE 4,4'-DIMETHYL
                                                                              ; P04166; 1B5M.
S0005055; CYB5.
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    Transmembrane; 37 HEME 1
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Last annotation update)
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  (BY SIMILARITY).
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Best Local :
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Eukaryota; Viridiplantae; Chlorellaceae; Chlorella.
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Q01170;
Q1-APR-1993
Nitrate
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BINDING
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CONFLICT
SEQUENCE
                                                      InterPro; IPR001199; -.

Pfam; PF00173; heme_1; 1.

Pfam; PF00174; oxidored_molyb; 1.

PROSITE; PS00191; CYTOCHROME_B5_1; 1.

PROSITE; PS00255; CYTOCHROME_B5_2; 1.

PROSITE; PS00255; MOLYBODYTERIN_EUK; PAF

PROSITE; PS00559; MOLYBODYTERIN, FAD; NAD;

Oxidoreductase; Flavoprotein; FAD; NAD;
                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                            EMBL; X56771; CAA40090.1; PIR; S17197; S17197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlorella nitrate reductase.";
Biochem. J. 278:203-209(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cannons A.C., Iida N., Solomonson L.F. "Expression of a cDNA clone encoding Chlorella nitrate reductase.";
                                                                                                                                                                                                     InterPro; IPR000572; -.
                                                                                                                                                                                                                            HSSP; P04166; 1B5M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STEP OF NITRATE ASSIMILATION IN PLANTS, FUNGI AND BACTERIA.

CATALYTIC ACTIVITY: NADH + NITRATE = NAD(+) + NITRITE + H(2)O.

COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD, HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME GROUP IS CALLED CYTOCHROME B-557.

SUBUNIT: HOMODYNERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS A CYTOCHROME B5 FAMILY, HEME-BINDING DOMAIN. SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE C-TERMINAL DOMAIN.
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                                                           Query Match
Best Local :
                                               Matches
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NON_TER
SEQUENCE
                                                                                                                       BINDING
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CYTOCHROME B5 (CYTB5).
                                                                                                                                                                   PRINTS; PR00363; CYTOCHROMEB5.1; PROSITE; PS00191; CYTOCHROME_B5_1; PROSITE; PS50255; CYTOCHROME_B5_2;
                                                                                                                                                                                                                                                                                                                                                                                                                       GUZOV V., FEYEREİSEN R.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYB5
                                                                                                                                                                                                                                  EMBL; L38464; AAA56985.1; HSSP; P04166; 1B5M.
                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                            SEQUENCE
                                                                                                                                                BINDING
                                                                                                                                                          Electron transport;
                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                               modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-RUTGERS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Musco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Musca domestica (House fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 IDATDEFNAIHSLKAKKQLLEYYIGELAEEGQEAAASDRA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 KDGTDVFDTFHPEAAWETLANFYVGDIDESDRDIKNDDFA 101
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                        w
                                                                                                                                                                                                                                                                                                          by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                             OXYGENASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APAGAKSETMAEV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAPSVRTFTRAEVLNAEALNEGKKDAEAPFLMIIDNKVYDVREFVPDHPGGS-VILTHVG
               AAPSVRTFTRAEVLNAEALNEGKKDAEAPFLMIIDNKVYDVREFVPDHPGG-SVILTHVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUSDO
SSEDVKYFTRAEV------AKNNTKDKNWFIIHNNVYDVTAFLNEHPGGEEVLIEQAG
                                                                                                                                                                                                            PF00173; heme_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34;
                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                      IPR001199; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muscidae; Musca
                                                                                                           134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    318
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318
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                                               Conservative
                                                                                                            Ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                       BELONGS TO THE CYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               274
318
                                                                                                                                                           Transmembrane; Heme;
                                                                                                           15401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.5%;
34.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34830
                                                          35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETHTTMESAW-FVVDGKVYDATPFLKDHPGGADSILLVAG 263
                                                                                                           MΨ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW;
                                                                                                                                                                                                                                                .
                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                        Score 130;
Pred. No. 0.
                                                                                                        POTENTIAL . 11A1A23E235EC3AA CRC64;
                                                                                                                                 HEME LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 135.5; DB Pred. No. 0.00056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEME LIGAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E60D82FE1E98292A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134
                                                                                                                                                                                                                                                                                                       There are no restrictions ng as its content is in
                                              es 35;
                                                                                                                                 (BY
                                                                     DB
                                                                                                                                                           Microsome
                                                                                                                                                                                                                                                                                                                                                                         B5 FAMILY.
                                                                                                                                 SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                              Usage
                                                                    Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                             Gaps
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EMBL; X16051; CAA34183.1; -
PIR; S06600; S06600.
HSSP; P00175; ILCO.
InterPro; IPR001262; -
InterPro; IPR001262; -
InterPro; IPR001199; -
Pfam; PF00170; FMN_dh; 1.
Pfam; PF00170; heme_l; 1.
PROSITE; PS00191; CYTOCHROME_B5_1; 1.
PROSITE; PS00191; CYTOCHROME_B5_2; 1.
PROSITE; PS00557; FMN_HYDROXY_ACID_DH; 1.
Electron transport; Respiratory chain; Ox
FMN; Heme; Mitochondrion; Transit peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1989 (Rel. 10, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-JCT-2000 (Rel. 40, Last annotation update)
CYTOCHROME B2 PRECURSOR (EC 1.1.2.3) (L-LACTATE DEHYDROGENASE
[CYTOCHROME]) (L-LACTATE FERRICYTOCHROME C OXIDOREDUCTASE) (L-LCR).
                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-90088451; PubMed-2688640;
Black M.T., Gunn F.J., Chapman S.K.,
"Structural basis for the kinetic di:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYB2_HANAN P09437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Amino-acid sequence of the cytochrome-b5-like heme-bi from Hansenula anomala flavocytochrome b2.";
Eur. J. Blochem. 169:539-546(1987).
-i- CATALYTIC ACTIVITY: L-LACTATE + 2 FERRICYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-88082787; Pub
Haumont P.-Y., Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Risler Y., Tegoni M., Gervais M.;
"Nucleotide sequence of the Hansenula anomala."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=90045973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetales;
NCBI_TaxID=4927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hansenula anomala (Yeast) (Candida Eukaryota; Fungi; Ascomycota; Sacch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1989
01-JAN-1990
                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                              entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       flavocytochromes b2 from the yeasts
Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             flavocytochrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                                               SIMILARITY: TO SPINAC P.PUTIDA S-MANDELATE
                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS: THIS
                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                            GROUPS
                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: HOMOTETRAMER
                                                                                                                                                                                                                                                                                                                                                              B5 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: MITOCHONDRIAL INTERMEMBRANE SPACE
                                                                                                                                                                                                                                                                                                                   2-MONOOXYGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 FERROCYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDATEHFEDVGHSSDAREMMKQYKVGELVAEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KDGTDVF-DTFHPEAAWETLANFYVGDIDESDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tochrome b2 (L-lactate:cytochrome Acids Res. 17:8381-8381(1989).
                                                                                                                                                                                                            requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80-163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263:973-976(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                              ΪN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=3319613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ascomycota; Saccharomycotina; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=2813072;
                                                                                                                                                                                                                                                                                                                               SPINACH GLYCOLATE OXIDASE (33% IDENTITY), TO DELATE DEHYDROGENASE, AND TO M.SMEGMATIS LACTATE
                                                                                                                                                                                                                                                                                                                                                                            THE N-TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                          ENZYME BINDS
   hain; Oxidoreductase; peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K., Reid G.A
differences
                                                                                                                                                                                                                                                                                                                                                                            SECTION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pelliculosa)
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                                                                                                                                                                                                                                                                                                                                                                                                          FMN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98
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                                                                                                                                                                                                                                                                                                                                                                              BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ala gene encoding
oxidoreductase).";
                                                                                                                                                                                                                                                                                                                                                                                                          PROTOHEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anomala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between
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                    Flavoprotein;
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                                                                                                                                                                                                                                                                                                                                                                            CYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                          PROSTHETIC
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Best Local S
Matches 36
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSIT
CHAIN
DOMAIN
BINDING
BINDING
Heme.
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation updat
                                   PROSITE;
                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                       CYM5_HUMAN
043169;
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                          Electron
                                                                                              EMBL; AB009282; BAA23735.1; HSSP; P04166; 1B5M.
                                                                                                                                                                                                                                                                                                                      CYTOCHROME B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
                                                           Pfam; PF00173; heme_1; 1.
PRINTS; PR00363; CYTOCHROMEB5.
                                                                                                                                                                                                                                                                                                                                                          rISSUE-Testis;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                    interPro; IPR001199; -.
                                                                                                                                                                                                                                                                                                                                                shibashi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 LFQSLGYYD-----SSKAYY 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70
                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY
                                                                                                                                                                                                                                                SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSQMINLHDFETIARQILPPPALAYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKDGTDVFDTFHPEAAWETLANF------YVGDIDESDRDIKND--DFAAEVRKLRT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTRAEV-----LNAEALNE-GKKDAEAPFLMIIDNKVYDVREFVPDHPGG-SVILTHV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKDATKIFVPIHPP----DTIEKFIPPEKHLGPLVGEFEQEEEELSDEEIDRLERIERKPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FISADVPHWKDIELTPEIVSQHNKKD---DLWVVLNGQVYDLTDFLPNHPGGQKIIIRYA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                         transport;
                                   PS00191; CYTOCHROME_B5_1; PS50255; CYTOCHROME_B5_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435
573 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74
74
80
115
138
432
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                                                                                                                                                                                                                                                                                                                                                                      N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        OUTER MITOCHONDRIAL MEMBRANE ISOFORM PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435
64202
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573
163
115
138
432
                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Primates;
                         Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MITOCHONDRION.
CYTOCHROME B2.
CYTOCHROME DOMAIN (CORE).
CYTOCHROME DOMAIN (CORE).
HEME LIGAND (BY SIMILARITY).
HEME LIGAND (BY SIMILARITY).
REMOVES THE SUBSTRATE ALPHA-PROTON AS THE
FIRST STEP IN CAPALYSIS (BY SIMILARITY).
SUBSTRATE BINDING (BY SIMILARITY).
MW; 83EEF645C580BC8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 128.5; DB Pred. No. 0.0044; 2; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209
                        Outer membrane; Transmembrane;
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01-FEB-1996
01-OCT-2000
TRANSMEM
SEQUENCE
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BINDING
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TRANSMEM
                                               PROSITE; PS00191; CYTOCHROME_B5_1; 1. PROSITE; PS50255; CYTOCHROME_B5_2; 1. Electron transport; Transmembrane; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Cuscuta reflexa (Southern Asian dodder).

Eukaryota; Viridiplantae; Embryophta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyjedons; core eudicots; Asteridae; euasterids

Solanales; Convolvulaceae; Cuscuta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CUSRE
                                                                                    PRINTS; PR00363; CYTOCHROMEB5.
                                                                                                                        EMBL; L22209; AAA62621.1;
HSSP; P04166; 1B5M.
                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                      modified and this statement is not removed.
                                                                                                                                                                                                    use
                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through
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-!- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
                                                                                                                                                                                                                                                                                                                                       haustoria formation in Cuscuta Gene 149:375-376(1994).
                                                                                                                                                                                                                                                                                                                                                               Subramaniam K., Mahadevan S.; "The cDNA sequence of cytochrome b5 associated with cytokinin-induced
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=95047507; PubMed=7959021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOCHROME B5
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                                                                                                           InterPro; IPR001199; -.
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Pred. No. 0.0011;
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HEME LIGAND (BY SIMILARITY)
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Query Match Best Local Similarity

5.1%; 46.7%;

Score 125; DB 1; Pred. No. 0.0014;

Length 135

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ch com time:	34 23	Matches
Search completed: Job time: 697 sec	MIIDNK :: LVIGGK	28;
Search completed: August 9, 2001, 20:36:48 Job time: 697 sec	34 MIIDNKVYDVREEVPDHPGGS-VILTHVGKDGTDVF-DTFHPEAAWETLANFYVGDIDES 91 :: : : : :	28; Conservative
01, 2	-VILT : : DVLLS	9;
0:36:48	HVGKDGTDVF-D7	9; Mismatches 21; Indels
	FHPEA ; ; [GHSSS	21;
	AWETLANFY ARAMMDEMC	Indels
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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ALIGNMENTS

A; Nedrus. A; Molecule type; DNA A; Residues: 1-197, 'VSHTFNN', 198-447 <WIL> A; Cross-references: EMBL: Z81122; PIDN: CAB('---+-1 source: Clone T13F2 FEBS Lett. 439, 215-218, 1998
A;Title: Functional identification of a fatty acid delta5 desaturase gene from Caenor A;Reference number: 222422; MUID:99059458
A;Accession: T43319
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-447 <MIC> A;Map position: 4
A;Introns: 43/3; 80/3; 197/3; 295/3; 318/2; 349/1; 384/3
A;Introns: 43/3; 80/3; 197/3; 295/3; 318/2; 349/1; 384/3
C;Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
C;Keywords: oxidoreductase; unsaturated fatty acid biosynthesis Qy В Qy 망 Q 뫄 A; Reference number: A; Accession: T24875 submitted to the EMBL Data Library, October 1996 A; Reference number: ${\tt Z19947}$ R;Michaelson, L.V.; Napier, J.A.; Lewis, M.; Griffiths, G.; Lazarus, C.M.; Stobart, FEBS Lett. 439, 215-218, 1998 C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000 C;Accession: T43319; T24875 δÃ A; Gene: CESP:T13F2.1; des-5 C; Genetics: A; Status: translated from GB/EMBL/DDBJ R; Swinburne, J. A;Cross-references: EMBL:AF078796; NID:g4003522; PIDN:AAC95143.1; PID:g4003523 C; Species: Matches Query Match Best Local Similarity 178 LFKNRYYNDLASYFVGNFLQGFSSGGWKEQHNVHHAATNVVGRDGDLDLVPFYATVAEHL 179 VFQDRFWGDLFGAFLGGVCQGFSSSWWKDKHNTHHAAPNVHGEDPDIDTHPL-LTWSEHA 124 fatty acid desaturase (EC 1.14.99.-) T13F2.1 [validated] - Caenorhabditis les: Caenorhabditis elegans 64 80 25 KKDAEAPFLMIIDNKVYDVREFV-PDHPGGSVILTHVGKDGTDVFDTFH---PEA-AWET 4 GSPLFYIRKI-----LETIFTILFAFYLQYHTY-YLPSAILMGVAWQQLGWLIHEFAHHQ SSKAYYAFKVSFNLCIWGLSTVIVAKWGQTSTLANVLSAALLGLFWQQCGWLAHDFLHHQ 178 LANFYVGDIDESDRDIKNDDF------------------AAEVRK----LRTLFQSLGYYD 118 ELKKECPTQEPEIPDIKDDPIKGIDDVNMGTFNISEKRSAQINKSFTDLRMRVRAEGLMD REQEHEPFFIKIDGKWCQIDDAVLRSHPGGSAITTYKNMDATTVFHTFHTGSKEAYQWLT 154; Conservative 25.5%; 76; Score 629; DB 1; Pred. No. 5.2e-45; 6; Mismatches 175 PIDN:CAB03352.1; GSPDB:GN00022; CESP:T13F2.1 175; Indels Length 447; 62; Gaps 177 123 63 13; eleg

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A;Introns: 13/3; 39/2; 234/3; 277/3; 378/1; 413/3
C;Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase C;Keywords: alternative splicing; oxidoreductase; unsaturated fatty
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A;Residues: 1-38,69-430,'V',432-473 <NAP>
A;Cross-references: EMBL:AF031477; NID:g3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Identification of a caenorhabditis elegans Delta6-fatty-acid-desaturase A;Reference number: Z21637; MUID:98149727 A;Accession: T37238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: clone W08D2
R; Napier, J.A.; Hey, S.J.; Lacey, D.J.; Shewry,
Biochem. J. 330, 611-614, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R:Swinburne, J.; Ainscough, R. submitted to the EMBL Data Library, March
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linoleoyl-CoA desaturase (EC 1.14.99.25) W08D2.4 - N;Alternate names: Delta6 fatty acid desaturase C;Specles: Caenorhabditis elegans C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000
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A; Accession: T26280
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                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                        LLGLFWQQCGWLAHDFLHHQVFQDRFWGDLFGAFLGGVCQGFSSSWWKDKHNTHHAAPNV 218
                                                                                                                                        MVESFEKLRQKLHDDGLMKANETYFLFKAISTLSIMAFAFYLQYLGW-----YITSAC
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                                  HGEDPDIDTHPLLTWSEHALEMFSDVPDEELTRMWSRF-----MVLNQTWFYFPILSFA
                                                                                                                                                                          LRTLFQSL------GYYDSSKAYYAFKVSFNLCIWGLSTVI-VAKWGQTSTLANVLSAA 158
                                                                                                                                                                                                            DATHIFHAFHEGSSQAYKQLDLLKKHGEHDEFLEKQLEKRLDKVDINVSAYDVSVAQEKK 131
                                                                                                                                                                                                                                               DGTDVFDTFHPEAAW------
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                                                                      LLALAWQQFGWLTHEFCHQQPTKNRPLNDTISLFFGNFLQGFSRDWWKDKHNTHHAATNV
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                                                                                                                                                                                                                                                                                                                                                   21.8%; Score 537; DB 1; 30.5%; Pred. No. 2.9e-37; Live 64; Mismatches 185
 -FAFIPG-DLCKYKASFEKAILKIVPYQHLYFTAMLPML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NID:g3088519; PIDN:AAC15586.1;
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A;Cross-references: EMBL:X87143; NID:g1040728; PIDN:CAA60621.1 (2)Superfamily: cytochrome b5 core homology C:Keywords: heme; iron; metalloprotein; oxidoreductase F:16-90/Domain: cytochrome b5 core homology <CB5> F;51,74/Binding site: heme iron (His) (axial ligands) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Delta8 sphingolipid desaturase (EC 1.14.99.-) [similarity] - C;SpecLes: Helianthus annuus (common sunflower) C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_chan C;Accession: S68358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-458 <SPE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ex;Sperling, P.; Schmidt, H.; Heinz, E. Eur. J. Blochem. 232, 798-805, 1995
A;Title: A cytochrome-b(5)-containing fusion
A;Reference number: S68358; MUID:96028121
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                                                                                                                                                                                                                                                                                                                                                              LTWSEHALEMFSDVPD----EELT-RMWSRFMVLNQTWFYFPILSFARLSWCLQSILFVL
                                                RHNFSKIQPAVETLCKKYNVRYHTTGMIEGTAEVFSRLNEVSKAA 450
                                                                                                                                                 IVFSLNHNGMPVISKEEAVDMDFFTKQIITGRDVHPGLFANWFTGGLNYQIEHHLFPSMP 405
                                                                                                                                                                                                                                                                                                                                                                                                                    GHDAGHYQMMATRGWNKFAGIFIGNCITGISIAWWKWTHNAHHIACNSLDYDPDLQHLPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AHDFLHHQVFQDRFWGDLFGAFLGGVCQGFSSSWWKDKHNTHHAAPNVHGEDPDIDTHPL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAGMFEKK----GHGVIYSLCFVSLLLSACVYGVLYSGSFWIHMLSGAILGLAWMQIAYL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLGYYDSSKAYYAFKVSFNLCIWG·-LSTVIVAKWGQTSTLANVLSAALLGLFWQQCGWL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVILTHV-GKDGTDVFDTFHPEAAWETLANFYVGDIDESDRDIKNDDFAAEVRKLRTLFQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NYQIEHHLEPSMPRHNESKIQPAVETLCKKYNVRYHTTGMIEGTAEVFSRLNEVSK 448
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RCHLRSISPICRELCKKYNLPYVSLSFYDANVTTLKTLRTAALQA 438
                                                                                                   IQFTLNHFSGDVYVGPPKGD-NWFEKQTRGTIDIACSSWMDWFFGGLQFQLEHHLFPRLP
                                                                                                                                                                                                                                                        PNGQAHKPSGARVPISLVEQLSLAMHWTWYLATMFLFIKDPVNMLVYFLVSQAVCGNLLA 345
                                                                                                                                                                                                                                                                                                           LAVSS----KLENSITSVFYGRQLTFDPLARFFVSYQHYLYYPIMCVARVNLYLQTILLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DAPLINLAGQDVTDAFIAFHPGTAWKHLDKLFTG---YHLKDYQVSDISRDYRKLASEFA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPSI-----EVLNSIA--DGKKYITSKELKKHNNPNDLWISILGKVYNVTEWAKEHPGG
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                                                                                                                                                                                                          -SKRKIPDRGLNILGTLIFWTWFPLLVSRLPNWP-ERVAFVLVSFCVTG-IQH
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Pred. No. 4.6e-
71; Mismatches
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A;Title: A sphingolipid desaturase from higher plants. Ide
A;Reference number: Z22986; MUID:99003197
A;Accession: T51848
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-449 <SPE>
A;Cross-references: EMBL.AJ224161; PIDN:CAA11858.1
A;Cross-references: EMBL.AJ224161; PIDN:CAA11858.1
A;Experimental source: cultivar Columbia; mainly green par C;Genetics:
A;Gene: sld1
A;Map position: 3
A;Note: F2A19.180
C;Function:
A;Description: (EC 1.14.99.-); delta-8 sphingolipid desatu C;Keywords: oxidoreductase; unsaturated fatty acid biosynt
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delta-8 sphingolipid desaturase (EC 1.14.99.-) [validated] - Arabidopsis thaliana delta-8 sphingolipid desaturase (EC 1.14.99.-) [validated] - Arabidopsis thaliana (Reconstruction of the construction                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
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A;Experimental source: cultivar Columbia; BAC clc
R:Sperling, P., Zaehringer, U; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
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ELCKKHNLPYRSMSWFE--ANVLT-INTLKTAA 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAFLGGVC-QGFSSSWWKDKHNTHHAAPNVHGEDPDIDTHPLLTWSEHALEMFSDVP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TFHPEAAWETLANFYVGDIDESDRDIKNDDFAAEVRKLRTLFQSLGYYDSSKAYYAFKVS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TEKKYITNEDLKKHNKSGD--LWIAIQGKVYNVSDWIKTHPGGDTVILNLVGQDVTDAFI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRAEVLNAEALNEGKKDAEAPFLMIIDNKVYDVREFVPDHPGG-SVILTHVGKDGTDVFD
                                                                  TLCKKYNVRYHTTGMIEGTAEVFSRLNEVSKAA 450
                                                                                                                                                                                                       ISKEEAVDMDFFTKQIITGRDVHPGLFANWFTGGLNYQIEHHLFPSMPRHNFSKIQPAVE 417
                                                                                                                                                                                                                                                                                 NFAGILVFWTWFPLLVSCLPNWPERF--FFVFTSFTVTALQHIQFTLNHFAADVYVGPPT
                                                                                                                                                                                                                                                                                                                                                   EQLSLAMHWTWYLATMFLFIKDPVNMLVYFLVSQAVCGNLLAIVFSLNH-----NGMPV 357
                                                                                                                                                                                                                                                                                                                                                                                                                      YDRKLTFDPVARELVSYQHFTYYPVMCFGRINLFIQTFLLLF-----SKREVPDRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -DEELT-RMWSRFMVLNQTWFYFPILSFARLSWCLQSILFVLPNGQAHKPSGARVPISLV 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQLLSGNCLTGISIAWWKWTHNAHHLACNSLDYDPDLQHIPVFAVS---TKFFSSLTSRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FVAAMF -- LGVLYGVLACTSVFAHQIAAALLGLLWIQSAYIGHDSGHYVIMSNKSY - NRF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FNLCIWGLSTVIVAKWGQTSTLANVLSAALLGLFWQQCGWLAHDFLHHQVFQDRFWGDLF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFHPGTAWHHLDHLFTG---YHIRDFQVSEVSRDYRRMAAEFRKLGLFENKGHVTLYTLA
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                                                                                                                                    DWFEKQAAGTIDISCRSYMDWFFGGLQFQLEHHLFPRLPRCHLRKVSPVVQ
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T50555

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delta-8 sphingolipid desaturase [imported] - rape C;Species: Brassica napus (rape) C;Jate: 21-Jul-2000 #sequence_revision 21-Jul-2000 #tex C;Accession: T50555
R;Sperling, P.; Zaehringer, U.; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A;Title: A sphingolipid desaturase from higher plants. A;Accession: T50555
A;Accession: T50555
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                               hypothetical protein At2g46210 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                  C; Genetics:
A; Gene: At2
                                                                                                                                                                                                                    R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Yanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-449 <SPE>
                                                                                   A; Molecule type: I
A; Residues: 1-449
                                                                                                                                                     A; Reference number: A84420; A; Accession: A84900
                                                                                                                                                                            A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thallana A; Reference number: A84420; MUID: 20083487
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                                                              A; Cross-references:
                                                                                                                                A; Status: preliminary
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At2g46210 osition: 2
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                                                              NID: g3702328; PIDN: AAC62885.1;
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Pred. No. 2.4e-34;
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linoleoyl-CoA desaturase (EC 1.14.99.25) [validated] - human N;Alternate names: Delta6 fatty acid desaturase; protein DKFZp58 C;Species: Homo sapiens (man) C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change C;Accession: T13155; T08765
                                                                               C;Superfamily: cytochrome b5 core homology C;Keywords: chromoprotein; heme; iron, met: F:18-94/Domain: cytochrome b5 core homolog; F:53,76/Binding site: heme iron (His) (axid
                                                                                                                                                            A; Cross-references: GD
A; Note: DKFZp586C201.1
                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 'RTRG',138-428,'D',430,'M',432-444 <WAM>
A; Cross-references: EMBL; ALO50118
A; Experimental source: adult uterus; clone DKFZp586C
                                                                                                                                                                                                                                                                                                                                     submitted to the Protein Sequence A; Reference number: Z16471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: Z17612; MUID:99085046
A;Accession: T13155
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A; Residues: 1-444 <CHO>
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J. Biol. Chem. 274, 471-477, 1999
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R;Aki, T.; Shimada, Y.; Inagaki, K.; Higashimoto, H.; Kawamoto, S.; Shigeta, Blochem. Biophys. Res. Commun. 255, 575-579, 1999
A;Title: Molecular cloning and functional characterization of rat delta-6 fat A;Reference number: JG0180; MUID:99160394
A;Accession: JG0180
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A;Residues: 1-444 <AKI>
A;Cross-references: DDBJ:AB021980; NID:g4514721; PIDN:BAA75496.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - C;Species: Rattus norvegicus (Norway rat) C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text.
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                                                                         SKAYYAFKVSFNLCIWGLSTVIVAKWGQTSTLANVLSAALLGLFWQQCGWLAHDFLHHQV 179
                                                                                                                                                                                                                             EGKKDAEAPF - - -
 FQDRFWGDLFGAFLGGVCQGFSSSWWKDKHNTHHAAPNVHGEDPDIDTHPLLTWSE----
                                                                                                              TDAFRAFHLDLDFVGKFLKPLLIGELAPEEPSLDRGKSSQITEDFRALKKTAEDMNLFKT
                                                                                                                                                 TOVFDTFHPEAAW--ETLANFYVGDIDESDRDI---KNDDFAAEVRKLRTLFQSLGYYDS 119
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                                                                                                                                                                                      EGSTELQAPMPTFRWEEIQKHNLRTDRWLVIDRKVYNVTKWSQRHPGGHRVIGHYSGEDA 68
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24.0%;
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N;Alternate names: delta6-desaturase
(;Species: Mucor rouxii
C;Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 31-Mar-2001
C;Accession: JC7556
R;Laoteng, K.; Mannontarat, R.; Tanticharoen, M.; Cheevadhanarak, S.
Bloothem. Bloophys. Res. Commun. 279, 17-22, 2000
A;Title: Delta6-desaturase of Mucor rouxii with high similarity to plant delta6-desatura
A;Reference number: JC7556; MUID: 20563795
A;Molecule type: DNA
A;Residues: 1-523 < CNA
A;Residues: 1-524 < CNA
A;Residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AR290983
A;Experimental source: strain ATCC 24905
C;Comment: This enzyme, a membrane-bound key
C;Keywords: transformation; oxidoreductase
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383 IEHHLFPTMPRHNLHKIAPLVKSLCAKHGIEYQEKPLLRALLDIVSSLKK 432
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NGMPVISKEEAVDMDFFTKQIITGRDVHPGLFANWFTGGLNYQIEHHLFPSMPRHNFSKI
                                                   NVRTRTLELVGITFFFVWFGSLLSTL-----PTWNIRIAYIMVSYMLTFPLHVQITLSH
                                                                                                                                                              NNIYSTYYKRVLPFDAASRFFVRHQHYLYYLILSFGRFNLHRLSFAYLL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EYGKKKLKYLPYNHQHEYFFLIGPPLLIPMYFQYQIIMTMIRRDWVDLAWAISYYARFF
                                                                                                     RVPISLVEQLSLAMHWTWY----LATMFLFIKDPV-NMLVYFLVSQAVCGNLLAIVFSLNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EIRTMHPPQVYEKLINLYCIGDYMPDVIRPASMKQQHTFTKPKEDKPVLTATWEGGFTVQ 13:
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Pred. No. 2.2e-28;
5; Mismatches 196;
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A; Nolecule type: DNA
A; Residues: 1-368 <TAS>
A; Cross-references: EMBL:X87094; NID:g809109;
A; Cross-references: constant of fatty
                                                                                                                                                                                                               linoleoyl-CoA desaturase (EC 1.14.99.25) - W;Alternate names: Delta6-desaturase C;Species: Spirulina platensis C;Date: 08-Jul-1995 #sequence_revision 21-C;Accession: S54809
                                                                                                                                               submitted to the EMBL Data A; Reference number: S54809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: T36617
R; Oliver, K.; Harris, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable Delta6 fatty acid desaturase (EC 1.14.99.-
C; Species: Streptomyces coelicolor
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: SCO
C;Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-345 <OLI>A; Cross-references: EMBL: AL078610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: Z21610
A; Accession: T36617
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                                                                                                  A; Status: preliminary
                                                                                                                            A; Accession: S54809
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les 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCOEDB: SCH35.42c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FANWFTGGLNYQIEHHLFPSMPRHNFSKIQPAVETLCKKYNVRYHTTGMI 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -PPGMAIAFLAVHQCLFGVYLGSAFAPNHKGMPILTADDR--PDFLRRQVLTSRNVNGGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YFPILSFARLSWCLQSILFVLPNGQAHKPSGARVPISLVEQLSLAMHWTWYLATMFLFIK 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLA---IAAFLAVMYGQVALVAHDMAHRQVFRRRRASELSGR-IAGASIGMSYGWWQDKH
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32.3%;
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              PIDN:CAA60573.1; acid biosynthesis
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                                   PID:9809110
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A;Cross-references: EMBL:D90914; GB:AB001339; NID:g1653477; PIDN:BAA18502.1; A;Experimental source: PCC 6803
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June C;Keywords: oxidoreductase; unsaturated fatty acid biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Reddy, A.S.; Nuccio, M.L.; Gross, L.M.; Thomas, Plant Mol. Biol. 22, 293-300, 1993
A;Title: Isolation of a Delta(6)-desaturase gene: A;Reference number: S35157; MUID:93283633
A;Accession: S35157
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R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Synechocystis sp.
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000 C;Accession: S35157; S76243
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                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-359 <KAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: S74322; A; Accession: S76243
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                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Sequence analysis of the genome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
                                                       180
                                                                                                                                       137 LSTVIVAKWGQTSTLANVLSA-----ALLGLFWQQCGWLA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 HIHYPKIAPILAEVCEEFGVNYAVHQT-FFGALAANYSWLKKMS 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137
96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RMSPSMEY-RWYHRY----QHWFIWFYYPFIPYYWSIADVQTMLFKRQYHDHEIPSPTWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDLFGAFLGGVCQ----GFSSSWWKDKHNT-HHAAPNVHGEDPDIDTHPLLTWSEHALEMF 241
           SSNPHINRVLGMTYDFV--GLSSFLWRYRHNYLHHTYTNILGHDVEIH------GDGAV
                                                   FQDRFWGDLFGAFLGGVCQGFSSSWWKDKHN-THHAAPNVHGEDPDIDTHPLLTWSEHAL 238
                                                                                             LKTLIIVLW-LFSAWAFVLFAPVIFPVRLLG-----CMVLAIALAAFSFNVGHDANHNAY 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHNFSKIQPAVETLCKKYNVRY--HTTGMIEGTAEVFSRLNEVS 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---VIEPAEFLDPDNLHIDDEWAIAQVKTTVDFAPNNPIINWYVGGLNYQTVHHLFPHIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GMPVISKEEAVDMD-----FFTKQIITGRDVHP-GLFANWFTGGLNYQIEHHLFPSMP 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PISLVEOLSLAMHWTWYLATMFLFIK-----DPVNMLVYFLVSQAVCGNLLAIVFSLNHN 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDVPDEELTRMWSRFMVLNQTWFYFPILSFARLSWCLQSILFVLPNGQAHK---PSGARV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKTAIILAWVVSAWTFVVFGPDVLWMKLLGCIVLGFGVSAVGFNISHDG-NHGGYSKYQW 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSTVIVAKW------GQTSTLANVLSAALLGLFWQQCGW-LAHDFLHHQVFQDRFW 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIATL----LAFKAFGVAVFLIIPIAVGYSPLEAVIGASIVYMTHGLVACVVFMLAH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-359 <RED>
                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                        8.5%;
25.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUID: 97061201
                                                                                                                                                                                    55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49;
                                                                                                                                                                                  Score 210.5; DB 2
Pred. No. 5.2e-10;
5; Mismatches 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 227; DB 2; Pred. No. 2.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the unicellular cyanobacterium Synechocysti
                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                    124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 368
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                                                                                                                                                                                  Indels
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                                                                                                                                         HDFLHHQV 179
                                                                                                                                                                               61;
                                                                                                                                                                               Gaps
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             146
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                                                                                                                                                                                                                                                                                                              June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synechocystis
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A;ACCESSACU. - A;A;ACCESSACU. - A;ACCESSACU. A;A;ACCESSACU. A;A;ACCESSACU. A;ACCESSACU. A;ACCESS
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R; Stover, C.K.; Pham, X.Q.;
adman, S.; Yuan, Y.; Brody,
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A82950; A; Accession: B83034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A;Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved hypothetical protein PA4888 [imported] - Pseudomonas aeruginosa C; Species: Pseudomonas aeruginosa
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                                     Query Match
Best Local 9
    Matches
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    Local Similarity
nes 80; Conserv
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    Conservative
                                     7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Erwin, A.L.; Mizoguchi, S.D.;
L.L.; Coulter, S.N.; Folger, I
    64;
Score 173.5; DB 2;
Pred. No. 6.9e-07;
4; Mismatches 142;
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                                                                           Length
    Indels
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K.R.; Kas,
                                                                                    370;
    95;
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    Gaps
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Larbig,
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                                   FSKIQPAVETLCKKYNVRYHT 429
                                                                                                                                                                                             SLAMHWTWYLATMFLFIKD----PVNMLVYFLVSQAVCGNLLA-----IVFSLNH 352
                                                                                                                                                                                                                                                                            MVLNQTWFYFPILSFARLSWCLQSILF----VLPNGQAHKPSGAR-----VPISLVEQL 306
                                                                                                                                                                                                                                                                                                                     ---PSDFWRHTHNHIHHTYTNVLGKDDDV------GYGVVRLFPE------QRWKPF 161
                                                                                                                                                                                                                                                                                                                                              QGFSSSWWKDKHN-THHAAPNVHGEDPDIDTHPLLTWSEHALEMFSDVPDEELTRMWSRF 256
                                                                                                                                                                                                                                                                                                                                                                                                                                     QTSTLANVLSAALLGLEWQQCG------WLAHDFLHHQ---VFQDREWGDLEGAELGGVC 197
YAALSREVREIARRYGQTYNS
                                                                                                                 NGMPVISKEEAVDMD----FFTKQIITGRDVHPGLFANWFTGGLNYQIEHHLFPSMPRHN 408
                                                                                                                                                          KLGROWT - - - - - - -
                                                                                                                                                                                                                                         YRWQPLWV-----
                                                                                                                                                                                                                                                                                                                                                                                                  PPTWL---LGSLLLGL-----GKILENMELGHNVMHGQYDWMNDPEFAGRAYEWDIAG-- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DRELTPEQLAAFGAELDALRLRTL-ADLG-ADDARYIRRVRAAVRVCCWSGRALLMFGWL 69
                                                                          TEKAVVFPPSVLEGETRGHWYLRQLRGSSNLEGGPLFHILTGNLSHQIEHHLYPDLPARR
                                                                                                                                                          -KDYLLFPLLGLFAGGFGAVFVGNLLANVLRNLWTFTVIFCGHF
                                                                                                                                                                                                                                       ----TLQALLFQYAVAIQHLRLDKYAKGRLDKAELMPLLRRLRA
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RESULT 15

results 15

results 15

cytochrome b5 [imported] - Arabidopsis thaliana
C;species: Arabidopsis thaliana (mouse-ear cress)
C;species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 01-Dec-2000
C;Accession: T52468
R;Fukuchi-Mizutani, M.; Mizutani, M.; Tanaka, Y.; Kusumi, T.; Ohta, D.
Plant Physiol. 119, 353-361, 1999
A;Title: Microsomal Electron Transfer in Higher Plants: Cloning and Heterolc A, Reference number: Z25274
A;Accession: T52468
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(;Species: Mycobacterium tuberculosis

(;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

(;Accession: G70590

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davles, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987

A;Accession: G70590
A; Molecule type: mRNA
A; Residues: 1-140 <FUK>
A; Cross-references: EMBL: AB007802; PIDN: CAB17232.1
A; Cross-references: EMBL: AB007802; PIDN: CAB17232.1
C; Superfamily: Cytochrome b5; cytochrome b5 core h
C; Keywords: heme; iron; metalloprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Pred. No. 1.8e-06;
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                                 core homology
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                                                                                                            67 VF-DTFHPEAAWETLANFYVGDIDESDRDI------KNDDFAAEVRKLR 108
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                                 TLFQSLG-----YYDSSKA 122
                                                                                                                                                   KVFTLSEV----SQHSSAKDC----WIVIDGKVYDVTKFLDDHPGGDEVILTSTGKDATD 57
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6; Mismatches 43;
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Search completed: August 9, 2001, 20:26:03 Job time: 242 sec

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  GenCore version 4.5 (c) 1993 - 2000 Compugen Ltd
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DEF1_LACLA
PEF2_LACLA
YOB1_CAEEL
NADE_MYCTU
CAN_DROME
RIP3_MOMCH
PSAD_SYNP6
AP19_YEAST
CALB_NEGGR
YMW3_YEAST
WODA_BPT4
RABB_DISOM
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Query Match Best Local s Matches 5

Similarity 100 5; Conservative

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commerc h/annour	h a collaboration EMBL outstation - trictions on its is in no way	D., Gocayne J.D., Reich C.I., , Glodek A., , Nguyen D., Hanna M.C., lovsky M., J.C.; Methanococcus				thermoactin saccharomyc xenopus lae archaeoglob escherichia streptococc aspergillus thermotoga herpesvirus campylobact saccharomyc sulfolobus

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"The DNA sequence of cosmid 14-13b from chromosome XIV of Saccharomyces cerevisiae reveals an unusually high number of overlapping open reading frames.";
Yeast 13:261-26(1997).
-1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND OXYGENASES. IT PLAYS A ROLE IN FATTY-ACID DESATURATION AND IS INVOLVED IN SEVERAL STEPS OF THE STEROL BIOSYNTHESIS PARHWAY, PARTICULARLY IN THE 4-DEMETHYLATION OF THE 4,4'-DIMETHYL
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Truan G., Epinat J.-C., Rougeulle C., Cullin C., Pompon D.;
"Cloning and characterization of a yeast cytochrome b5-encoding
which suppresses ketoconazole hypersensitivity in a NADPH-P-450
reductase-deficient strain.";
                                                                                                                                                               PROSITE; PS00191; CYTOCHROME_B5_1; 1.

PROSITE; PS50255; CYTOCHROME_B5_2; 1.

Electron transport; Transmembrane; Heme;
BINDING 37 37

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CONFLICT 17 17 E -> Q (IN F
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MEDLINE=97245296; PubMed=9090055;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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RESULT 4

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ID CY51_ARATH STANDARD; PRT; 134 i

AC Q42342; Q9SB05;

DT 01-0CT-2000 (Rel. 40, Created)

DT 01-0CT-2000 (Rel. 40, Last sequence updated)

DT 01-0CT-2000 (Rel. 40, Last sequence updated)

CYTOCHROME B5 ISOFORM 1.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Embryophyta; Tra

OC Magnoliophyta; eudicotyledons; core eudico

OC Brassicales; Brassicaceae; Arabidopsis.
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-I- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROT FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE OXYGENASES (BY SIMILARITY).
-I- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO
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PRINTS; PR00363; CYTOCHROMEB5.
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Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND OXYGENASES (BY SIMILARITY).
                                           Eukaryota; Viridiplantae; Embryophyta; Magnoliophyta; eudicotyledons; core euc Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                             BRAOL
                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001199; -. Pfam; PF00173; heme_1; 1. PRINTS; PR00363; CYTOCHROMEB5
                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00191; CYTOCHROME_B5_1; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
Electron transport; Transmembrane; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a or send an email to
SEQUENCE FROM N.A., AN STRAIN-CV. CAULIFLORA
                                                                               Brassica oleracea
                                                                                                       CYTOCHROME
                                                                                                                                                                CYB5_BRAOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mendel; 6696; Arath;1218;6696.
HSSP; P00171; 1CYO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heterologous expression Arabidopsis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fukuchi-Mizutani M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=9880378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                  NCBI_TaxID=3712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Microsomal electron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                1 KVYDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Ewropean Bioinformatics Institute. There are no restruct by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY:
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                                                                                                                                                                                                                          KVYDV
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5; Conserv
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ilarity 100.0%;
Conservative (
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31, Last sequ.
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                                                                                (Cauliflower).
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sion of NADH-cy
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            SEQUENCE OF
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fer in higher plants: cloning
   NADH-cytochrome beta5 reduct;
                                                                                                                 sequence update) annotation update)
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                                                                                                                                                                                                                                                                      Score 26; DB
Pred. No. 32;
0; Mismatches
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9CC01C60f7C873FD CRC64;
                                                                                                                                                                PRT;
            6-47
                                                         eudicots;
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                                                        Tracheophyta; S
dicots; Rosidae;
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RESULT 6
CYB5_C
CYB5_C
AC P49097
AC P49097
O1-FEB
DT 01-FCB
DT 01-CCT
OC CUSCUT
OC EUKary
OC EUKary
OC Magnol
OC Solana
OX NCBI_T
RN [1]
RN [1]
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RR SEQUEN
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BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Brassica Olerace Plant Physiol. 99:1254-1257(1992).
-!- FUNCTION: CYTCCHROME B5 IS A MEMBRANE BOUND
                                                                                                       "The cDNA sequence of cytochrome haustoria formation in Cuscuta re Gene 149:375-376(1994).
-!- FUNCTION: CYTOCHROME B5 IS A FUNCTION AS AN ELECTRON CARRI
                                                                                                                                                                                                                                       Cuscuta reflexa (Southern Asian dodder).
Eukaryota; Viridiplantae; Embryophyta; Tracheo
Magnoliophyta; eudicotyledons; core eudicots;
Solanales; Convolvulaceae; Cuscuta.
                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel.
01-FEB-1996 (Rel.
01-OCT-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                               CYB5_CUSRE P49097;
                                                                                                                                                                       Subramaniam K., Mahadevan S.;
                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                            NCBI_TaxID=4129;
                                                                                                                                                                                                                                                                                            CYTOCHROME B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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PRINTS; PR00363; CYTOCHROMEB5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
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                                                                                                                                                                                      MEDLINE=95047507;
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                                                                                                                                                                                                                                                                                                                                                                                                                               29
                                                 SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (B SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (B'SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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                                                                                             OXYGENASES.
               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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  Bioinformatics
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                                                                                                        IS A MEMBRANE BOUND CARRIER FOR SEVERAL
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reflexa.";
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                                                                  TO THE SIMILARITY)
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dae; euasterids
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RESULT 7
CYBS_T
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DT 01-FEB
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CC SOLBAR
OX MEDLL
RP SEQUEN
RA SMITLL
RT VITCO
CC -1-FL
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P49098;
01-FEB-1996
01-FEB-1996
01-OCT-2000
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                                                     modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restues by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94325476; PubMed=8049375;
Smith M.A., Stobart A.K., Shewry P.R.,
"Tobacco cytochrome b5: CDNA isolation,
vitro protein targeting.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOCHROME B5
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PRINTS; PR00363; CYTOCHROMEB5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4097;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KVYDV 5
                                                                                                                                                                                                                                                                                                                                       THE DEVELOPING SEED IS UTILIZED FOR MEMBRANE SYNTHESIS AND IN THE DEVELOPMENTALLY REGULATED PRODUCTION OF LARGE AMOUNTS OF STORAGE LIPIDS. IS INVOLVED IN THE REDUCTION OF CYTOCHROME P-450 AND MAY THEREFORE BE INVOLVED IN FLAVONOID BIOSYNTHESIS IN THE PETALS SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY). TISSUE SPECIFICITY: IS HIGHLY EXPRESSED IN DEVELOPING SEEDS, MODERATELY EXPRESSED IN FLOWERS, AND IS EXPRESSED AT LOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nt Mol. Biol. 25:527-537(1994).

FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND OXYGENASES. MAY PLAY A KEY ROLE IN THE MODIFICATION BY DESATURATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH IN
                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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| KVYDV 32
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PS50255; CYTOCHROME_B5_2; 1.
transport; Transmembrane; Heme;
39 39 HEME LIGAND
63 63 HEME LIGAND
106 126 POTENTIAL.
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(Rel. 33, Last sequence update)
(Rel. 40, Last annotation update)
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14745 MW;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Napier J.A.;
                                                                                                                                       There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
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Q10343;
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Q1-OCT-1996
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Pfam; PF00173; heme_1; 1.
PriNTS; PRO0363; CYTOCHROMEB5.
PROSITE; PS00191; CYTOCHROME_B5_1;
PROSITE; PS50255; CYTOCHROME_B5_2;
PROSITE; PS50255; CYTOCHROME_B5_2;
PROSITE; PS50255; Transmembrane;
NEME;
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CONFLICT
CONFLICT
                                                                                                   NON_TER
SEQUENCE
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                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                   MCLean J., Harris D., Barrell B.G., Rajandream M.A., Walsh S.V.; Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL PROTEIN C1F12.01C IN CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                        Hypothetical protein
                                                                                                                                    Pfam; PF00571; CBS; 3.
                                                                                                                                                           EMBL; 269944; CAA93805.1;
                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                        -!- SIMILARITY: BEL
SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                     STRAIN-972;
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                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces.
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HSSP; P04166; 1B5M.
                                                                                                                                                InterPro;
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203
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274 AA;
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Pred. No. 64;
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LA -> EF (
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Pred. No. 32;
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MISSING (IN CAA48240).
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SIMILARITY).
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RESULT

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TRXB_AQUAE

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RESULT 10 FLAD_RHIME
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Best Local Similarity
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30-MAY-2000
30-MAY-2000
FLAGELLIN D.
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                                                                                                           FLAD_RHIME Q52942;
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DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aquitex aeolicus.
Bacteria; Aquific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRXB OR AQ_500.
                   Rhizobium meliloti (Sinorhizobium meliloti). Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae; Sinorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
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30-MAY-2000
                                                     FLAD
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                                                                                                                                                                                                                                                                                                                                                 PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98196666; PubMed-9537320;
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                                                                                                                                                                            11 KVYDV
                                                                                                                                                                                                 1 KVYDV 5
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SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
MISCELLANEOUS: THE ACTIVE SITE IS A REDOX-ACTIVE DISULFIDE BOND.
SIMILARITY: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: REDUCED THIOREDOXIN.
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                                                                         (Rel. 39, (Rel. 39, (Rel. 39,
                                                                                                                                                                                                                                                                               323 AA;
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143
155
276
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Last
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(EC 1.6.4.5) (TRXR).
                                                                                                Created)
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NAD(P) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
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Pred. No.
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                              Rhizobiaceae group,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Platzer J., Schmitt R.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYM
FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
-i- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
PHYTOENE SYNTHASE PRECURSOR (EC 2.5.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00700; Flagellin_C;
Pfam; PF00669; Flagellin_N;
Flagella; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: 2 GERANYLGERANYL
PREPHYTOENE DIPHOSPHATE.
-!- CATALYTIC ACTIVITY: PREPHYTOENE DIPHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Magnoliophyta;
Andropogoneae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L49337; AAB81421.1; -. InterPro; IPR001029; -.
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                                                                                                                                                                                                                                                    -!- PATHWAY: CAROTENOID BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=96304610; PubMed=8722797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4577;
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SIMILARITY: BELONGS TO THE PHYTOENE/SQUALENE SYNTHETASE FAMILY
                                                                                                                                                                                                                                                                                                      PHYTOENE.
                                                                                                                                                                                                                                                                                                                                                                                                    TO PHYTOENE
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5; Conserv
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Zea.
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; Poales; Poaceae; PACC clade; Panicoideae;
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                                       http://www.isb-sib.
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P53797;
01-0CT-1996 (Rel. 3
01-0CT-1996 (Rel. 3
15-JUL-1998 (Rel. 3
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Pfam: pF00494; SQUALEN_PHYTOEN_SYN_1; 1.

PROSITE; PS01044; SQUALEN_PHYTOEN_SYN_2; 1.

Multifunctional enzyme; Carotenoid biosynthesis;

Multifunctional enzyme; Carotenoid biosynthesis;

Isoprene biosynthesis; Transferase; Chloroplast; Transit CHLOROPLAST (POTENTIAL).
                                                                                                                                                                                                     This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSY.

Narcissus pseudonarcissus (Daffodil).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Eukaryota; Viridiplantae; Embryophyta; Amaryllidaceae; Narcissus.
                     Multifunctional enzyme; Carotenoid biosynthesis; Isoprene biosynthesis; Transferase; Chloroplast; Transit peptide. TRANSIT 136 CHLOROPLAST (POTENTIAL).
 SEQUENCE
               CHAIN
                                                            InterPro; IPR002060; -.
Pfam; PF00494; SOS_PSY; 1.
PROSITE; PS01044; SQUALEN_PHYTOEN_SYN_1; 1.
PROSITE; PS01045; SQUALEN_PHYTOEN_SYN_2; 1.
                                                                                                               EMBL; X78814; CAA55391.1; -.
                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                           Schledz M.,
                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Paracorolla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=39639;
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                                                                                                                                                                                         European
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                                                                                                                                                                                                                                                                   SUBUNIT:
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                                                                                                                                                                                                                                                                                                                      PREPHYTOENE DIPHOSPHATE
                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: 2 GERANYLGERANYL DIPHOSPHATE
                                                                                                                                                                                                                                                                                                                                              TO PHYTOENE
                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: CHLOROPLAST
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                                                                                                                                                                                                                                                                                                                                                                                            of a Narcissus pseudonarcissus cDNA for phytoene
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N -> T (IN ALLELE B73)
21070A33624EED79 CRC
              PHYTOENE SYNTHASE
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Pred. No.
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Mismatches
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BINDING
SEQUENCE
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Pfam; PF00585; Thr_dehydrat_C; 2.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
Isoleucine biosynthesis; Lyase; Mitochondrion;
                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a obstween the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                               transformation marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; I
Saccharomycetales;
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15-DEC-1998
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                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                         -!- COFACTOR: PYRIDOXAL
-!- PATHWAY: FIRST STEP
                                                                                                                                                                                                                                                                                                                                                                                                                   Yeast 14:1017-1025(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wartmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98398049; PubMed=9730281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=37620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arxula adeninivorans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THDH_ARXAD
                                                                                                                                                                                                                InterPro; IPR000634;
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"AILV1 gene from the yeast Arxula
48
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                     1 KVYDV 5
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PATHMAY: FIRST STEP OF ISOLEUCINE BIOSYNTHESIS.
SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
SUBCELLULAR LOCATION: MITOCHONDRIAL.
SIMILARITY: TO THREONINE DEHYDRATASE CATABOLIC
                                                                                                                                                                                                                                                                                                                                 DEHYDRATASE.
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KVYDV
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5; Conserv
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                                                                                                                                     peptide.
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 52
                                          Conservative
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37,
37,
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60416
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RESULT

DPOL_BPPRD

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Query Match
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01-JUL-1989
15-DEC-1998
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"Site-specific mutagenesis of PRDI DNA polymerase: mutations in highly conserved regions of the family B DNA polymerase.";

Biochem. Biophys. Res. Commun. 170:1294-1300(1990).

-i- FUNCTION: THIS POLYMERASE POSSESSES TWO ENZYMATIC ACTIVITIES:
DNA SYNTHESIS (POLYMERASE) AND AN EXONUCLEOLYTIC ACTIVITY THA DEGRADES SINGLE STRANDED DNA IN THE 3' TO 5' DIRECTION.
-i- CATALYTIC ACTIVITY: N DEGXYNUCLEOSIDE TRIPHOSPHATE =
N PYROPHOSPHATE + DNA(N).
                                                                                                                                                                                                  EMBL; M69077; AAA32456.1;
EMBL; J03018; AAA32452.1;
EMBL; M22161; AAA32450.1;
EMBL; X06321; CAA29637.1;
                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=88067710; PubMed=3684578;
Hsieh J.-C., Jung G., Leavitt M.C., Ito J.;
"Primary structure of the DNA terminal protein of bacteriophage PRDI.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete nucleotide sequence of the left very early region of Escherichia coli bacteriophage PRD1 coding for the terminal protein and the DNA polymerase.";
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Bacteriophage PRD1.
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DNA POLYMERASE (EC
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Jung G., Leavitt M.C., Hsieh J.-C., Ito J.;
"Bacteriophage PRDI DNA polymerases: evolution of DNA polymerases.";
Proc. Natl. Acad. Sci. U.S.A. 84:8287-8291(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P10479;
                                                                                              DNA-binding; Hydrolase; Exonuclease.
                                                                                                              Transferase; DNA-directed DNA polymerase; DNA replication;
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PROSITE; PS00116; DNA_POLYMERASE_B; 1.
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MEDLINE-90358833; PubMed-2202298;
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                                                                                                                                                         InterPro; IPR002064; -.
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                                                                                                                                                                                                                                                                                                                                 European Bioinformatics Institute.
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A39970; A39970.
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0LIGOENDOPEPTIDASE F, F
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CONFLICT
SEQUENCE
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                                                                                ACT_SITE
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METAL
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                                                                                                                                                                                                                                                                           SEQUENCE FROM N. STRAIN-NCDO 763;
                                                                                                                       Pfam; PF01432; Peptidase_M3; 1.
PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
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MEDLINE=95096044; PubMed=7798200;
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terization of PepF, an oligopeptidase
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Search completed: August 9, 2001, 20:36:49 Job time: 698 sec



GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

OM protein protein search, using sw model

August 9, 2001, 20:26:04; Search time 50.69 Seconds (without alignments) 7.514 Million cell updates/sec

Title: Perfect score: 1 KVYDV 5 US-09-367-013B-2_COPY_39_43 26

Scoring table:

Gapop 10.0 , Gapext 0.5 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database PIR_68:*
1: pir1:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

C;Accession: PQ0816 J.M.; Kwon, O.Y.; Kim, Y.S.; Lee, D.S.; Cho, M.J.; Lee, H.H.; Nam Plant Physiol. 103, 359-370, 1993
A;Title: Generation of expressed sequence tags of random root cDNA clones of Brassica A;Reference number: PQ0816; MUID:94302145
A;Accession: PQ0816 A;Molecule type: mRNA
A;Residues: 1-51 <CAR>
A;Experimental source: root, cv. Naehan
C;Superfamily: cytochrome b5; cytochrome b5 core homology
F;1-51/Domain: cytochrome b5 core homology (fragment) <CB5> probable cytochrome b5 - rape (fragment)
C;Species: Brassica napus (rape)
C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 20-Apr-2000 Query Match Best Local S Matches y Match 100.0%; Score 26; Local Similarity 100.0%; Pred. No. hes 5; Conservative 0; Mismatch 1 KVYDV 5 core 26; DB 2; Length 51; red. No. 20; Mismatches 0; Indels 0, 0

Db 2 KVYDV 6

hypothetical protein MJ0916 - Methanococcus jannaschii C; Species: Methanococcus jannaschii C; Species: Methanococcus jannaschii C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1998 C; Accession: D64414 R; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak R; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak R; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak R; Bult, C.J.; White, O.; Olsen, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996 R.A.C.; Cotton, M.D.; Fraser, C.M.; Smith, H.O.; Woese A; Althors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc A; Accession: D64414

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA A; Residues: 1-89 <BUL>

A;Cross-references: GB:U67535; GB:L77117; NID:g1591586; PID:g1591589; TIGR:MJ0916; PI 。 Genetics:

A:Map position: REV847877-847608 C:Superfamily: hypothetical protein MJ0916

Query Match
Best Local Similarity 100.0%; Score 26; Pred. No. 36; 2; Length 89;

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RESULT
T40071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: electron transfer C; Superfamily: cytochrome b5; cytochrome b5 core homology C; Keywords: electron transfer; heme; iron; metalloprotein; transmembrane
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R;d'Antoni, A.; d'Angelo, M.; dal Pero, F.; Sartorello, F.; Pandolfo, D.; Lanfranchi, submitted to the EMBL Data Library, February 1996
A;Description: The DNA sequence of cosmid 14-13b from chromosome XIV of Saccharomyces
                                            A; Reference number: Z21903
A; Accession: T40071
                                                                                     R; Lyne, M.; Rajandream, M.A.; submitted to the EMBL Data Lil
                                                                                                                             cytochrome b5 - fission yeast (Schizosaccharomyces pombe)
c;Species: Schizosaccharomyces pombe
C;Date: 03-Dec:1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
C;Accession: T40071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 149, 123-127, 1994
A;Title: Cloning and characterization of a yeast cytochrome b(5)-encoding gene which A;Reference number: S47919; MUID:95047457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:Z71387; NID:g1302031; PIDN:CAA95990.1; PID:g1302032; A;Experimental source: strain S288C R;Truan, G.; Epinat, J.C.; Rougeulle, C.; Cullin, C.; Pompon, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 20-Jun-2000 C;Accession: S63052; S47919; S67347
                            A;Status:
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A; Accession: S67347
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A; Accession: S63052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytochrome b5 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein N1949; protein YNL111
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A; Residues: 1-16,'Q',18-120 <TRU>
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cule type: DNA
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nes 5; Conserv
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                      preliminary; translated from GB/EMBL/DDBJ
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ite: heme iron (His) (axial ligands) #status
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                                                                                     Barrell, B.G.;
brary, December
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Pred. No.
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RESULT
T14454
A;Description: acts as electron carrier for membrane-bound oxygenases C;Superfamily: cytochrome b5; cytochrome b5 core homology C;Keywords: electron transfer; heme; iron; membrane protein; metalloprotein F;5-80/Domain: cytochrome b5 core homology <CB5> F;40,64/Binding site: heme iron (His) (axial ligands) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytochrome b5 - wild cabbage
C;Specles: Brassica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
C;Accession: T1454
R;Kearns, E.V.; Keck, P.; Somerville, C.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:AB007801; PIDN:CAB17231. C;Superfamily: cytochrome b5; cytochrome b5 core C;Keywords: heme; iron; metalloprotein
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C;Accession: 
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T52469
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                                                                                                                                                                                                A;Cross-references: EMBL:M87514; NID:g167139; PID:g167140 C;Function:
                                                                                                                                                                                                                                                                       A;Status: preliminary;
A;Molecule type: mRNA
A;Residues: 1-134 <KEA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, March 1992 A; Description: Nucleotide sequence of cDNA for cytochrome
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A; Residues: 1-134 <FUK>
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A; Accession: T52469
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Pred. No.
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Mismatches
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Query Match

100.0%;

Score

26;

DB 2;

Length 134

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28

KVYDV

32

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C;Keywords: electron transfer; heme; iron; membrane protein; metalloprotein F;4-79/Domain: cytochrome b5 core homology <CB5> F;39,63/Binding site: heme iron (His) (axial ligands) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                   R;Subramaniam, K.; Mahadevan, S. Gene 149, 375-376, 1994
A;Tille: The cDNA sequence of cytochrome b5 associated with cytokinin-induced haustoria A;Reference number: Z16903; MUID:95047507
A;Accession: T09946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Cuscuta reflexa (southern Asian dodder) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 C;Accession: T09946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytochrome b5 - southern Asian dodder C; Species: Cuscuta reflexa (southern
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Best Local Similarity
"~+~hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziai Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallor ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:L22209; NID:g450584; PIDN:AAA62621.1; PID:g450585 C;Function:
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                                                                                                                                                                                                                                  A;Description: acts as electron carrier for membrane-bound oxygenases C;Superfamily: cytochrome b5; cytochrome b5 core homology
                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNAA;Residues: 1-135 <SUB>
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C; Superfamily: cytochrome b5; cytochrome b5
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A;Residues: 1-135 <STO>
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                                                                     Query Match
Best Local
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                                                                     100.0%; Score 26; 100.0%; Pred. No.
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Pred. No.
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Mismatches
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R;Le, T.; Weinstock, L.; Rifkin, L. submitted to the EMBL Data Library, May 1997 A;Description: The sequence of C. elegans co A;Reference number: Z18308
                                                                                                                                                                probable cytochrome b5 W02D3.1 {similarity} - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Co-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
C;Accession: T15210
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C;Superfamily: cytochrome b5; cytochrome b5 core homology
C;Superfamily: heme; iron; metalloprotein
C;Reywords: heme; iron; metalloprotein
F;40,64/Binding site: heme iron (His) (axial ligands) #status
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R;Fukuchi-Mizutani, M.; Mizutani, M.; Tanaka, Y.; Kusumi, T.; Ohta, D.
Plant Physiol. 119, 353-361, 1999
A;Title: Microsomal Electron Transfer in Higher Plants: Cloning and Heterologous
A;Reference number: Z25274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytochrome b5 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 01-Dec-2000
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A;Accession: S46306
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A; Residues: 1-140 <FUK>
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A; Residues: 1-139 <SMI>
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C;Superfamily: cytochrome b5; cytochrome b5 core homology C;Keywords: heme; iron; metalloprotein F;4-82/Domain: cytochrome b5 core homology <CB5> F;4-82/Domain: cytochrome b5 core homology <CB5>
                                                                                A; Residues: 1-151 <BEV>
                                                                                                                      A; Reference number: Z15419
A; Accession: T05600
                                                                                                                                                         R; Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Holsubmitted to the Protein Sequence Database, February
                                                                                                                                                                                                                     probable major latex protein F9D16.150 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_chan
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C:Superfamily: wound-induced protein Sn-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein At2g01520 [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001 C:Accession: G84425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-141 <LET>
                                     A;Cross-references: EMBL;AL035394
A;Experimental source: cultivar Columbia; BAC clone F9D16
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A; Introns: 31/3
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A; Map position:
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A; Residues: 1-151 <STO>
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A; Accession: G84425
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Pred. No. 59;
Mismatches
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Pred. No.
                                                                                                                                                             Wambutt, R.; Hoheisel,
tabase, February 1999
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R;Grellet, F.; Cooke, R.; Laudie, M.; Raynal, M.; Delseny, M. submitted to the EMBL Data Library, October 1995
A;Reference number: S71257
A;Accession: S71257
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A; Introns: 28/3; 106/1; 185/3; 210/3
                                                                                                                                                                                                                              A;Cross-references: EMBL:292826; PIDN:CAB07320.1; GSPDB:GN00021; CESP:C18D11.1 A;Experimental source: clone C18D11
                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-263 <WIL>
                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, March 1997
A;Reference number: Z19118
A;Accession: T19387
                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein C18D11.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T19387
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A; Residues: 1-155 <GRE>
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Copyright (c) 1993 - 2000 Compugen
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sp_bacteria:*
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7.599 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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263	212	212	155	155	151	151	142	141	140	135	135	134	132	128	124	117	51	Length
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Q9xy48 ctenocepnal Q9xtz4 caenorhabdi		Q9v6k5 drosophila	Q39132 arabidopsis	082979 bacillus sp	Q9suq9 arabidopsis	Q9zvf3 arabidopsis	O66353 unidentifie	001816 caenorhabdi	Q9zwt2 arabidopsis	Q9fdw8 arabidopsis	Q9gv21 polyandroca	O48618 olea europa	024651 olea europa	Q38634 bacteriopha	094391 schizosacch	Q9w419 drosophila	Q9s993 brassica na	Description

RESULT Q9W419

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Q9v8u7 drosophila	Q9w7s0 anguilla an .	Q9ey54 vibrio sp.	P96168 vibrio harv	Q9kg92 bacillus ha	Q9v0il pyrococcus	Q9gnq7 leishmania	Q50838 methanococc		Q9znw2 physcomitre	Q91em9 ceratodon p	Q9k8p6 bacillus ha	Q9flp4 arabidopsis	Q9hey1 mortierella	Q9hey4 mortierella	Q9uvv3 mortierella	Q9uvy3 mortierella	Q9ycs5 aeropyrum p	Q9zrp8 brassica na	O82348 arabidopsis	Q9mbd4 petunia hyb		Q9k703 bacillus ha	O66836 aqulfex aeo	Q20355 caenorhabdi	Q9kah0 bacillus ha

ALIGNMENTS

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MEDLINE=94302145; PubMed=8029332;

MEDLINE=94302145; PubMed=8029332;

Park Y.S., Kwak J.M., Kwon O.Y., Kim Y.S., Lee D.S., Cho M.J.,

Lee H.H., Nam H.G;

"Generation of expressed sequence tags of random root cDNA clones of generation of expressed sequence tags of random root cDNA clones of Brassica napus by single-run partial sequencing.";

Blant Physiol. 103:359-370(1993).

-I-SIMILARITY: TO CYTOCHROME B5 DOMAIN.
                                                                                                                                       Heme.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9S993 PRELIMINARY; PRT; 51 AA. Q9S993; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) CYTOCHROME B5 HOWOLOG (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                     Brassica napus (Rape).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                  InterPro; IPR001199; -.
InterPro; IPR001199; -.
Pfam; PF00173; heme_1; 1.
PRINTS; PR00363; CYTOCHROMEB5.
PROSITE; PS50255; CYTOCHROME_B5_2;
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3708;
                                                                                                                                                                                                                                 HSSP; P04166;
2 KVYDV
                              1 KVYDV 5
                                                           Similarity 5; Conserva
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                                                                                                                                        51 AA;
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                                                                                                                                        5609 MW;
                                                           Score 26; DB Pred. No. 79; O; Mismatches
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkóv B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Sylrekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang S.H., Zhong F.N., Rhong W., Zhou X., Zhan M., Zhang G., Zhao Q., Zheng L.,
The genome sequence of Drosophila melanogaster.";
RT The genome sequence of Drosophila melanogaster.";
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Q9W419;
01-MAY-2000
01-MAY-2000
01-MAR-2001
                                                                                                                                                                  Heme.
SEQUENCE
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Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tarcheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscr

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                          -1- SIMILARITY: TO CYTOCHROME B5 DOMAIN.
EMBL; AE003437; AAF46141.1; -
HSSP; P04166; 1BSM.
F1yBase; FBgn0029854; CG3566.
                                                                                                                                                                                                                         PRINTS; PR00363; CYTOCHROMEB5
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                                                                                                                                                                                                                                                         nterPro; IPR001199; -.
 26
                                     1 KVYDV .5
   KVYDV 30
                                                                                                                                                                                                                                          PF00173; heme_1; 1
                                                                                                                                                                                                    PS50255; CYTOCHROME_B5_2; 1.
                                                                                                                                                                    117
                                                                         Conservative
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Pred. No.
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                                                                         Mismatches
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RESULT
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Q38634;
01-NOV-1996
01-NOV-1996
01-NOV-1996
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094391;
01-MAY-1999
01-MAY-1999
                                                                                                      Poglazov A.B., Porter D., Kutter E.M., Mesyanzhinov V.V.; Submitted (CCT-1995) to the EMBL/GenBank/DDBJ databases. EMBL; L46838; AAA74682.1; -. EMBL; L46834; AAA74674.1; -. EMBL; L46834; AAA74674.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BINDING
BINDING
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                                                                                                                                                                                                                                                                                                                                             FRD2.
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PRINTS; PR00363; CYTOCHROMEB5.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lyne M., Rajandream M.A., Barrell B.G., Lelaure V., Galibert F.; Submitted (DEC-1998) To the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROBABLE CYTOCHROME SPBC29A10.16C.
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                                                                                                                                                                                                                                                                              Viruses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: MICROSOMAL CYTOPLASMIC SIDE OF THE ENDOPLASM EMBL; AL034463; CAA22444.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=972;
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                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      NCBI_TaxID=42177,
                                                                                                                                                                                                                                                                                                 Bacteriophage LZ6,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Electron transport; Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27
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    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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62
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                                                                                                                                                                                                                                                            42175;
                                                                                                                                                                                                                                                                                                 and Bacteriophage LZ1
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13910 MW;
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62
                       100.0%;
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Pred. No. 2e+
0; Mismatches
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                     Score 26; DB 9;
Pred. No. 2.1e+02;
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    Mismatches
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                                                                                                                              STRAIN-CV. KORONEIKI;
Martinkovskaya A.I.;
Submitted (NOV-1997)
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Magnoliophyta; eudicotyledons;
Lamiales; Oleaceae; Olea
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Olea europaea (Common olive).
Diea europaea (Common olive).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
STRAIN-CV. KORONEIKI;
Martsinkovskaya A.I., Poghosyan
Hatzopoulos P., Muzphy D.J.;
Submitted (NOV-1997) to the EMBI
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PRINTS; PR00363; CYTOCHROMEB5.
PROSITE; PS00191; CYTOCHROME_1
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Magnoliophyta; eudicotyledons;
Lamiales; Oleaceae; Olea.
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PROSITE; PS50255; CYTOCHROME_B5_2;
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dons; core eudicots; Asteridae;
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Q9GV21;
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SEQUENCE FROM N.A. Yamada K., Liu S.X., Toriumi M., Yu G., B
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SEQUENCE
                                                                                                PUTATIVE CYTOCHROME T1K7.28.
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PRINTS; PR00363; CYTOCHROMEB5.
PROSITE; PS00191; CYTOCHROME_B5_1;
PROSITE; PS50255; CYTOCHROME_B5_2;
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EMBL; AJ001370; CAA04703.1; -
HSSP; P04166; 1B5M.
Mendel; 27871; Oleea;1218;27871.
InterPro; IPR001199; -
                                                      Eukaryota; Viridiplantae; Embryophyta; Trache Magnoliophyta; eudicotyledons; core eudicots; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                             Q9FDW8
                                                                                                                                                                                                                                                                                                              Submitted (MAY-2000) to the EMBL; AB042613; BAB17853.1; SEQUENCE 135 AA; 15465 MW
                                          NCBI_TaxID=3702;
                                                                                      Arabidopsis thaliana (Mouse-ear cress)
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NCBI_TaxID=7723;
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TOCHROME B5 PROTEIN (TIK7.28 PROTEIN).
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dicots; Rosidae; eurosids II;
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01-MAY-1999 (TrEMBLrel.
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CYTOCHROME B5.
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"The sequence of BAC T1K7 from Arabidopsis thaliana chromosome 1.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF332415; AA648778.1; -
EMBL; AC013427; AAF98581.1; -
EMBL; AC013427; AAF98581.1; -
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Eukaryota; Viridiplantae; Embryophyta; Trachec
Magnoliophyta; eudicotyledons; core eudicots;
Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                            EMBL; AB007802; CAB17232.
EMBL; AB012242; BAB09434.
HSSP; P04166; 1B5M.
                                                                                                                                                                                                                                                                 Sequence features of the regions of 1,36 physically assigned P1 and TAC clones."; DNA Res. 5:203-216(1998).
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Chin C., Chiou J., Choi E., Chung M.,
Vaysberg M., Altafi H., Brooks S., Bue
Conway A.B., Hansen N.F., Johnson-Hops
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Southwick A., Da
         SEQUENCE
                                                 Pfam; PF00173; heme_1; 1.

PRINTS; PR00363; CYTOCHROMEB5.

PROSITE; PS00191; CYTOCHROME_B5_1;

PROSITE; PS50255; CYTOCHROME_B5_2;
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Kotani H., Nakamura Y., Sato S., Asamizu E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-99097071; PubMed-9880378; Fukuchi-Mizutani M., Mizutani M.,
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STRAIN=CV. COLUMBI
                                                                                                                                                Mendel; 34947; Arath;1218;34947.
InterPro; IPR001199; -
                                                                                                                                                                                                                                                                                                             "Structural analysis of Arabidopsis thaliana chromosome 5. VI. Sequence features of the regions of 1,367,185 bp covered by 19 physically assigned P1 and TAC clones.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heterologous expression of NADH-cytochrome beta5 reductase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fukuchi-Mizutani M., Mizutani M., Tanaka Y., Kusumi T., Microsomal electron transfer in higher plants: cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Davis R.W., Ecker J.F
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                                                                                                                                                                                                                     BAB09434.1; -.
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         15097 MW;
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Johnson-Hopson C., Khan S., Kim C., L
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Last sequence up
Last annotation
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Pred. No. 2
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         18C24FF8F7995E08 CRC64;
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Davis R.W.,
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Matches 5; Conser
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001816;
01-JUL-1997
01-JUL-1997
01-MAR-2001
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Sunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
                                                                                                                 PROSITE;
                                                                                                                                                         Submitted [3]
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=BRISTOL N2; Le T., Weinstock L.,
                                                                                                                                     InterPro; IPR001199; -.
Pfam; PF00173; heme_1; 1
                                                                                                                                                                                                                                                                                                            elegans
                                                                                                                                                                                                                                                                                                                     Watson A., Weinstock L., Wilkinson-Sproat
"2.2 Mb of contiguous nucleotide sequence
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MEDLINE=94150718; PubMed=7906398;
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Rhabditidae; Peloderinae;
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                                                                                                        Heme.
                                                                                                                                                                                                                                                                                                 Nature 368:32-38(1994).
 31
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KVYDV
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                                         Similarity 5; Conserv
                                                                                                               PS00191; CYTOCHROME_B5_1; PS50255; CYTOCHROME_B5_2;
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 35
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                                         Score 26; DB Pred. No. 2.3 0; Mismatches
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Pred. No.
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2.3e+02;
                                                    2.3e+02;
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RESULT 13
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AC Q9SUQ9
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 Q9SUQ9
Q9SUQ9;
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01-NOV-1999 (TrEMBLrel. 10, Last sequence upontative Major Latex Protein.
F219.14.
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01-AUG-1998
01-AUG-1998
01-OCT-2000
                                                                                                                                                            STRAIN-CV. COLUMBIA;
ROUNSley S.D., Lin x., Kaul S., Shea T.P., Fujii C.Y., M
Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Ven
"Arabidopsis thaliana chromosome II BAC F2I9 genomic seq
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005560; AAC67328.1;
Mendel; 33968; Arath;1544;33968.

SEQUENCE 151 AA; 17513 MM; C8D237FA88EFAECB CRC64;
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NON_TER
SEQUENCE
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Ohkuma M., Noda S., Kudo T.,
Submitted (MAR-1998) to the
EMBL; AB011937; BAA28471.1;
HSSP; P00456; 1CP2.
                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                   Q9ZVF3
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PRINTS; PR00091; NITROGNASEII.
PROSITE; PS00746; NIFH_FRXC_1;
PROSITE; PS00692; NIFH_FRXC_2;
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(Trembirel. 07, Last sequence update)
(Trembirel. 15, Last annotation update).
IT OF DINITROGENASE REDUCTASE (FE PROTEIN) (FRAGMENT).
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15173 MW;
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0; Mismatches
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Pred. No. 2.5
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            PRT;
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082979;
01-NOV-1998 (TrEMBLrel. 0
01-NOV-1998 (TrEMBLrel. 0
01-NOV-1998 (TrEMBLrel. 0
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Bevan M., Wedler H., Wedler !

Mayer K.F.X., Schueller C.;

Mayer K.F.X. (FEB-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
Wedler H.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of
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Eukaryota; Viridiplanttae; Embryophyta; Trache;
Magnoliophyta; eudicotyledons; core eudicots;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                 gene.";
Submitted (JUN-1998) to the
EMBL; AB015670; BAA31536.1;
SEQUENCE 155 AA; 17953 MW
                                                                                                                                                                                                                                "Alkalophilic Bacillus gene.":
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Ohdan K., Kuriki T
                                                                                                                                                                                                                                                                                                                   Bacillus/Staphylococcus
NCBI_TaxID=1409;
                                                                                                                                                                                                                                                                                                                                                        Bacillus sp.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EU Arabidopsis sequencing pr
Submitted (MAR-2000) to the
EMBL; AL035394; CAA23034.1;
EMBL; AL161559; CAB79323.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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bmitted (FEB-1999) to the EMBL/GenBank/DDBJ
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KVYDV
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Conservative
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Pred. No. 2.5
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Pred. No. 2.5e+02;
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2.5e+02;
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O39132

O39132;
AC O39132;
DT O1-NOV-1996 (TrEMBLICEL. 01, Created)
DT O1-NOV-1996 (TrEMBLICEL. 01, Last sequence update)
DT O1-NOV-1996 (TrEMBLICEL. 01, Last sequence update)
DT O1-NOV-1999 (TEMBLICEL. 12, Last annotation update)
DT O1-NOV-1999 (TEMBLICEL. 12, Last annotation update)
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DE EMBLICATION (TEMBLICEL. 12, Last annotation update)
OC Brasicales: Tracheophyta: Spermatophyta:
DC Eukaryota; Viridiplantae; Embryophyta: Tracheophyta: Spermatophyta:
DC Endstryota; Viridiplantae; Endstryophyta: Spermatophyta:
DC Endstryota; Viridiplantae; Endstryophyta: Spermatophyta: Spermatophyta:
DC Endstryota; DC Endstryota; Spermatophyta: Spermatophyta: Spermatophyta: Spermatophyta: Spermatophyta: Spermatophyta: Spermato
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Result
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Maximum DB seq length: 2000000000
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Perfect score:
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          110
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                                                                                                                                                                                                                                    Score
        A_Geneseq_0601:*

1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*

2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*

3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*

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Match Length
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Gapop 10.0 ,
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Copyright (c) 1993 - 2000 Compugen Ltd
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AAB11403
AAR65097
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AAY29303
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AAW42450
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Biotinylation pept
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AAB40091 AAG07990	AAY13084	90	AAG19062	AAG18777	AAY58783	AAG32672	AAG35333	AAY69169	AAG27099	AAY48225	AAG27110	AAG16088	AAB55892	AAY75953	AAB64683	AAY83230	AAW83944	AAG19063	AAG27909	AAY83242	AAY83241	AAY83236	AAY83235	AAY48336	AAB31651	AAY83232	AAY83231	AAG35334	271	579	1219	AAB31646
Anti-hIL12 antibod Arabidopsis thalia	Human secreted pro	Arabidopsis thalia	Zea mays protein f	Zea mays protein f	e DAHP synthet	mays protein	protein	human	5	O	pro	Arabidopsis thalia	ll protein	skin cel	ecreted	CYB5RP f	n secreted pr	Zea mays protein f	g	5 desti	ty acid	lower hy	fatty a	Human prostate can	sec	e bi	5RP fa	mays protein	ıys protei	Human secreted pro	nte	Amino acid sequenc

ALIGNMENTS

AAR12709

AAR12709 standard; Protein;

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31-JUL-1991 AAR12709;

(first entry)

Pentapeptide paralogue for use as chromatographic affinity ligand

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HPLC.
                         Identifying paralog with specific affinity for analyte - using candidate paralogs with systematically varied values of at least
                                             WPI; 1991-163985/22.
                                                                                                                                          Synthetic.
                                                           Kauvar LM;
                                                                        (TERR-) TERRAPIN TECHN INC.
                                                                                     31-OCT-1989;
                                                                                                   31-OCT-1990;
                                                                                                                 16-may-1991.
                                                                                                                              WO9106356-A.
                                                                                     89US-0429721
                                                                                                  90WO-EP06333
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Claim 41; Fig 8; 95pp; English.

2 parameters.

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Best Local Similarity
Thes 4; Conserv
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harvested from mice and used to provide a panel of antibody-secreting hybridoma cells as a subset of the complete B-cell repertoire). Nearly uniform binding to all antibody members of the repertoire was observed. The test was than repeated with the addition of a defined amount of analyte to the mixture. A small number of wells showed greatly decreased labelling and these antibodies represented the successful result of an initial screen for those which preferentially bind analyte.
                                                                                                                    A panel of 88 pentapeptides was designed on the basis of decreasing hydrophobicity and periodic variation of hydrophobic moment. The peptides were labelled with iodine-125 and tested with individual members of a basal antibody repertoire. (Spleen cells were
                                                                                                                                                                                                                        Screening of candidate drugs for binding comparing inverse image antibody profile mimotype-binding profile of receptor
                                                                                                                                                                                             Example 3; Fig 3; 29pp; English.
                                                                                                                                                                                                                                                                                    WPI; 1994-109390/13
                                                                                                                                                                                                                                                                                                                 Kauvar LM
                                                                                                                                                                                                                                                                                                                                                                         06-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                       13-OCT-1987;
11-OCT-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5300425-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       screening assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mimotope peptide #67 from panel of maximally diverse mimotopes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR51573 standard; peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide is one of a panel, each of which have systemicly varied values of at least two parameters. A test protein is matched against the panel, and the paralogues with highest binding affinity are selected. Selected paralogues are bound to a matrix which is incorporated into the HPLC gel and used as affinity ligands.
                                                                                                                                                                                                                                                                                                                                            (TERR-) TERRAPIN TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                 13-OCT-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       panel; rational drug design;
g assay; hydrophobicity; antil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; ilarity 100.0%; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                      87US-0108130.
88US-0255906.
89US-0447009.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "acetylated"
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AA
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Pred. No. 3.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody repertoire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      candidate drug;
                                                                                                                                                                                                                                       of to
                                                                                                                                                                                                                                      drug with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 5;
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RESULT
AAR69941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                          11-OCT-1988;
13-OCT-1987;
04-JUN-1993;
                                AAR69875-969 are pentameric mimotopes designed on the basis of decreasing hydrophobicity and periodic variation of hydrophobic moment. All the pentapeptides are acetylated at the N-terminus except E12 (for FITC) (sic). E12 is not identified in the specification. The mimotopes are used in the method of the invention to obtain antibodies specifically and strongly reactive with a desired analyte. The mimotope is obtd. by reacting a panel of starting a mammal with an analyte (so as to identify a malyte-reacting Abs) and then reacting each of a panel of candidate mimotopes representative of a random set of 3D contours with the analyte-reacting Abs. A subject is immunised with one or more mimotopes identified and the
                                                                                                                                                                                                                                            Producing antibodies with high specificity and affinity for an analyte - by immunisation with selected mimotope, also analyte detection kits, useful for immunoassay of materials usually
                                                                                                                                                                                                                                                                                                 WPI; 1995-105497/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mimotope; antibody; production; high specificity; detection;
immunoassay; high performance liquid chromatography.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
Sequence
                         product Abs are
                                                                                                                                                                                                                                                                                                                                                                                                                              13-OCT-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pentameric mimotope 67 used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR69941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR69941 standard;
                                                                                                                                                                                                                                                                                                                                                  (TERR-) TERRAPIN TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity hes 4; Conserv
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                                                                                                                                                                                                                                  by HPLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G
                                                                                                                                                                                                      Fig 3;
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87US-0108130.
93US-0072190.
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                          recovered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                        25pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Acetyl-Asn"
                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 27;
Pred. No.
                        the serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        obtain highly specific antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 15;
                         subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 5;
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Query Match

100.0%;

Score

27;

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16;

Length 5;

100.0%;

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RESULT
AAR98687
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                    The present peptide is a member of a panel of 88 pentapeptide minotopes designed on the basis of decreasing hydrophobicity, and periodic variation of hydrophobic moment. The panel was synthesised using the method of Geysen, H. M., et al, Proc. Natl. Acad. Sci. USA (1984), which uses lots of 96 pins; the remaining 8 polyethylene pins being controls. The minotopes were then mixed, 22 labelled and tested with individual members of a basal antibody (Ab) repertoire. Nearly uniform binding to all members was found. The test was then repeated with the addition of a defined ant. of analyte. A small number showed greatly increased labelling, these Ab representing the successful result of an initial screen for those that pref. bind analyte. The above is an example of a claimed method for identifying members of a panel of candidate drugs, that bind to a receptor having a known ligand. It is useful in rational drug design, e.g. selection of immunological reagents for any analyte, including those not normally detectable by immunoassay, e.g trace contaminants in soil,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100 Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-DEC-1989;
13-OCT-1987;
11-OCT-1988;
08-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Panel; mimotope; decreasing hydrophobicity; periodic variation; hydrophobic moment; antibody; repertoire; identification; drug; candidate; receptor; binding; liquand; rational; design; selectitiesent; tumour; production; immunological reagent; analyte;
                                                                                                                                                                                                                                                                                                         Example 3; Fig 3; 27pp;
                                                                                                                                                                                                                                                                                                                                                      Identifying competitive
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-361955/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-OCT-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUL-1996
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Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KAUV/) KAUVAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            trace contaminant; mimetope
                                                                                                                                                                                                                                                                                                                                                   candidate drugs that bind a specific receptor by reaction with panel of mimetope(s) - useful in re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89US-0447009.
87US-0108130.
88US-0255906.
93US-0118133.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "acylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 member diverse mimotope panel
                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 3.4e+05;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                    rational
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                            Matches
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                                     Query Match
Best Local S
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Best Local
                                                                                                                          (CDRs) carrying a cysteline noose and which have cytokine agonist and antagonist mechanisms of action. The method of the invention can be used to obtain peptide ligand mimetics capable of binding a target antigen. The binding members may also be used to provide agonists or antagonists of targets such as cytokines. In particular specific binding members for MIP-1 alpha receptors are useful for treatment of HIV infection and for in vitro investigation of mechanisms of HIV infection and for peptide ligand mimetics from CDR3 cysteine noose libraries provide a means to select a different and potentially more effective population of peptide ligands than direct display of similar cysteine noose ligands on the surface of bacteriophage. The products of the invention have anti-HIV activity. ANOB352-Y08378 and ANY08382-Y08398 are peptides used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cysteine noose; antibody variable domain; CDR; cytokine; agonist; complementarity determining region; antagonist; mimetic; antigen; MIP-1 alpha receptor; treatment; HIV infection; CDR3; anti-HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                        Sequence
                                                                                                                   'n
                                                                                                                                                                                                                                                                                                This invention describes the construction of libraries of antibody
                                                                                                                                                                                                                                                                                                                          Example
                                                                                                                                                                                                                                                                                                                                                 Cysteine noose antibody libraries
                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-313343/26
                                                                                                                                                                                                                                                                                                                                                                                                      Osbourn
                                                                                                                                                                                                                                                                                                                                                                                                                              (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cysteine noose library SCFV VH CDR3 clone MI1 peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY08373 standard; Protein;
                                                                                                                                                                                                                                                                                   variable domains containing modified complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1999
                                                                                                                   the
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  1 HPGG
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                                                                                                                   method
                            4;
                                      Similarity
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                                                                                                                                                                                                                                                                                                                          Page 41;
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ت
                            Conservative
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                                                                                                                   of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-GB03255
                                                                                                                                                                                                                                                                                                                       64pp;
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                                        100.0%;
                                                                                                                    invention
                                                                                                                                                                                                                                                                                                                          English.
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                            0;
                                        Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 27; DB 17;
Pred. No. 3.4e+05;
Mismatches 0;
                          red. No. 49;
Mismatches
                                                                                                                                                                                                                                                                                                                                                   and their production
                                                    20;
                            0;
                                                    Length 14;
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                            Indels
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RESULT
AAB11403
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                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                               This invention describes novel nucleic acid sequences from alkane metabolizing Candida yeasts, encoding cytochrome b5-polypeptide, its fragments, variants and mutations. The nucleic acids and polypeptides are used for the oxidation of long-chain alkyl compounds with at least 10C, and for the production of long-chain dicarbonic acids by oxidizing n-alkanes and fatty acids with at least 10C.
            Misc-difference
                                             Synthetic
                                                                  biotinylation; peptide; recombinant; fusion specific; defined; purification; BirA; enzym
                                                                                                   Random biotinylation peptide 62
                                                                                                                                                 AAR65097;
                                                                                                                                                                     AAR65097 standard; Peptide;
                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1.2; Page 6; 27pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid sequences from alkane metabolizing Candida yeast, encoding cytochrome b5 and used for the oxidation of long chain alkyl compounds and for the production of long chain dicarbonic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-679674/66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200065061-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Candida maltosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytochrome b5; alkane long-chain dicarbonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ი
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB11403 standard; peptide; 15 AA
                                                                                                                          25-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schunck W, Chernogolov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DELB-)
                                                                                                                                                                                                                                                                       Local Similarity nes 4; Conserv
                                                                                                                                                                                                                            11 hpgg 14
                                                                                                                                                                                                                                                  1 HPGG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  maltosa
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                                                                                                                                                                                                                                                                                                                               15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytochrome
                                                                                                                                                                                                                                                                      100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000WO-DE01246
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                                                                                                                         (first entry)
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           Location/Qualifiers 6
/note= "encoded by a supE suppressed amber codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           metabolism; oxidation; long-chain alkyl compound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide fragment T53.
                                                                                                                                                                      22
                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                Score 27;
Pred. No.
                                                                                                                                                                      A
                                                                  enzyme;
                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                            21;
                                                                            protein;
                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                           Length 15;
                                                                                                                                                                                                                                                                       Indels
                                                                             small;
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RESULT
AAW46700
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Best Local :
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                                                                                                                                                                            Biotinylation peptide; biotinylation enzyme; biotin-protein ligase; BirA; biotin ligase; biotin; purification; immobilisation; labelling; detection; protein; melrose binding protein; MBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A host cell, eg. E. coli is transformed with the fusion gene and is cultured in the presence of biotin and a biotinylation enzyme, eg. B. This library was used to explore the general utility of biotinylated peptides and to expand their possible uses.
WPI; 1998-178542/16
                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                           Biotinylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR65091-106 are biotinylated peptides that were designed to fit the consensus sequence of the invention and a random peptide (AAR65090). The library was made so that the biotinylyation peptides would be expressed in a fusion protein at the N-terminus of cytoplasmic MBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; Page 137; 146pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Production of biotinylated proteins by expression of recombinant DNA vector - which encodes a fusion prote comprising a protein and a biotinylated peptide.
                      Schatz PJ;
                                           (AFFY-) AFFYMAX TECHNOLOGIES NV
                                                                 30-JUL-1993;
                                                                                       03-FEB-1995;
                                                                                                             03-MAR-1998
                                                                                                                                  US5723584-A.
                                                                                                                                                                                                                                                28-MAY-1998
                                                                                                                                                                                                                                                                      AAW46700;
                                                                                                                                                                                                                                                                                           AAW46700 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-090609/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AFFY-) AFFYMAX
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                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                          peptide expressed at the N-terminus of MBP.
                                                                 93US-0099991.
                                                                                       95US-0383753.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "biotin-Lys"
                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 27;
Pred. No.
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                                                                                                                                                                                                                                                                                            B
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                                                                                                                                                                                                                                                                                                                                                                                                        73;
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RESULT
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Best Local
                                                                                                                                                                                                               03-FEB-1995;
30-JUL-1993;
28-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptides AAW46694-709 are non-naturally occurring biotinylation peptides, derived from a library constructed to express peptides of the sequence AAW46693. The library was made so that the biotinylation peptides are expressed in a fusion protein at the N-terminus of cytoplasmic melrose binding protein (MBP). The ability to express functional biotinylation sequences free at either end of a protein indicates that there is no requirement that either end of the peptide free in order to interact with the biotin holoenzyme synthetase. The peptides can be biotinylated in vitro or in vivo, especially with BirA biotin ligase, and used for the purification, immobilisation, labelling
biotinylation of proteins synthesized by recombinant DNA techniques in vivo with a biotinylation peptide of less than 50 amino acids. The method comprises: (a) on the surface of a substrate, providing a fusion protein comprising a recombinant protein and a peptide defined by the
                                                                                                 Identification and biotinylation of proteins synthesized recombinant DNA techniques in vivo
                                                                                                                                                                                                                                                                                                                                                                                       Biotinylation enzyme; biotin-protein ligase; BirA; labelling; biotin carboxyl carrier protein; BCCP; Escherichia coli;
                                                                                                                                                                                                                                                                                                                                                                                                                             Biotinylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY29303 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                  The present invention describes a method for the identification
                                                                            Claim
                                                                                                                                        WPI; 1999-457113/38
                                                                                                                                                                                         (AFFY-) AFFYMAX TECHNOLOGIES
                                                                                                                                                                                                                                                                 28-OCT-1997;
                                                                                                                                                                                                                                                                                           03-AUG-1999
                                                                                                                                                                                                                                                                                                                  US5932433-A
                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                     Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                              fusion
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                                                                            6;
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A
                                                                                                                                                                                                                                                                                                                                                                                                                            peptide
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93US-0099991.
97US-0959512.
                                                                            68;
                                                                                                                                                                                                                                                                 97US-0959512
                                                                                                                                                                                                                                                                                                                                                                     carrier protein; BCCP; Escherighia coil;
identification; purification; diagnosis; research.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide;
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                                                                          35pp; English
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Pred. No.
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RESULT 1
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Best Local S
Matches 4
This invention describes novel nucleic acid sequences (A) that are expressed at high level in normal prostatic tissue. Polypeptides (I) encoded by (A) are used: (a) for identifying agents for treatment of prostatic cancer and (b) for therapy of prostate cancer, optionally where expressed by gene therapy methods. (A) is also used to isolate full-length genes (for gene therapy) and for recombinant production of (I), which can be used to raise specific antibodies. (A) are identified by assembly of ESTs (expressed sequence tags) before these are analyzed for expression pattern (tissue specificity). This approach eliminates many of the false results, as regards tissue specificity, associated with known methods that use single (usually short) ESTs. ANY48304-Y48456 represent peptides encoded by the expressed sequence tags described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biotinylated by a biotin ligase at the lysine residue adjacent to position 8 and is 13-50 as in length; (b) in a predefined region of the substrate, contacting the fusion protein with an enzyme; and (c) determining whether the fusion protein has been biotinylated. The method allows the identification and purification of biotinylated enzymes e.g. BirA. The method is also useful in research and diagnostic applications. The method uses small but specific peptides, allowing the labelling of a protein at a defined site, this provides improved immobilization and avoids the use of antibodies. AAY2443 to AAY2458, and AAY2929 to AAY29312 represent specifically claimed examples of biotinylation peptides for use in the method of the invention.
                                                                                                                                                                                                                                                                                                               WPI; 1999-519629/44.
N-PSDB; AAZ33504.
                                                                                                                                                                                                                  Claim 22;
                                                                                                                                                                                                                                                       New nucleic acid expressed encoded polypeptides, used agents
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                                                                                                                                                                                                                                                                                                                                                              Specht T,
                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expressed sequence tag; EST; prostate; tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY48362 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                             (META-) METAGEN GES GENOMFORSCHUNG MBH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue
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                                                                                                                                                                                                               146; 194pp; German.
                                                                                                                                                                                                                                                                                                                                                            Hinzmann B,
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Pred.
                                                                                                                                                                                                                                                                 high level in normal prostatic treat cancer and screen for the
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76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatment; gene therapy;
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AAW42450
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Best Local
      fertile, transgenic plant whose genome has been augmented relative to that of the corresponding non-transgenic recipient cells through the stable introduction of the polynucleotide composition. The invention provides for the identification of DNA segments encoding the fungal pheromones, and compositions comprising pheromone polypeptides, which inhibit fungal growth and development and prevent or reduce fungal infection and/or disease in plant host cells. Also provided are methods and processes utilising fungal pheromone and pheromone derivatives in the prevention and treatment of fungal colonisation of a plant.
                                                                                                                                                                                    This is a MFalphal mating pheromone from Cryptococcus neoformans used in the preparation of a transgenic plant with increased resistance to fungal infections. The transgenic plant's genome is augmented by the introduction of a fungal pheromone gene, which confers resistance to fungal infection. The transgenic plant is prepared by a process which comprises obtaining a polynocleotide composition comprising 1 or more functions.
                                                                                                                                                                                                                                                                                                                      Transgenic plant, whose genome contains a fungal pheromone gene has increased resistance to fungal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cryptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C. neoformans MFalphal mating pheromone used in a transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW42450 standard; peptide;
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                                                                                                                                                          fungal pheromone genes, contacting recipient plant cells with the polynucleotide composition, regenerating plants from recipient cells
                                                                                                                                                                                                                                                                                            Example 5;
                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-063072/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cleavage-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cryptococcus
                                                                                                                           which have received the polynucleotide composition and identifying a fertile, transgenic plant whose genome has been augmented relative to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15
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4; Conser
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                                                                                                                                                                                                                                                                                          Page 98; 141pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                           Ebbole DJ,
Zhang L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "predicted peptide cleavage site involved
in pheromone maturation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mating; transgenic plant; fungal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention
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                                                                                                                                                                                                                                                                                                                                                                                                           Kazmierczak P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 27; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA
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82;
                                                                                                                                                                                                                                                                                                                                                                                                             Mccabe
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RESULT 1 AAB12198 ID AAB1

AAB12198 standard; peptide; 41 AA.

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Best Local S
Matches 4
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Best Local Similarity
                                                                                                                                                                The specification describes an immunogenic epitope of a Mycobacterium vaccae antigen. The epitope is a stimulator of cytokine production. The epitopes are useful for threatment of immune disorders, infectious diseases, especially tuberculosis, and cancer. They are also useful for treatment of other mycobacterial infections such as those caused by Mycobacterium avium. The epitopes are especially useful those caused by Mycobacterium avium.
                                                                                                                                                                                                                                                                                   Novel polypeptides comprising immunogenic epitopes of Mycobacterium vaccae, useful for treating mycobacterial infections, immune disorder and cancers
                                                                                                                                                                                                                                                                                                                                  WPI; 2001-168411/17
N-PSDB; AAF25077.
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                                                                                                                Sequence
                                                                                                                                                                                                                                                        Claim 1; Page 70; 80pp; English.
                                                                                                                                                                                                                                                                                 and cancers
                                                                                                                                                                                                                                                                                                                                                                        Delcayre
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29-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium vaccae
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                                                                                                                                          present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200104140-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; mycobacterial infection; TH1 immune response; vaccine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of a M. vaccae immunogenic epitope from DNA27
                                                                                                                                                       for inducing TH1
                                                                                                                                                                                                                                                                                                                                                                                                 (GENE-) GENESIS RES & DEV CORP LTD
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                                                   Local Similarity
nes 4; Conserv
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                          1 HPGG 4
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                                                   100.0%; ilarity 100.0%; Conservative (
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99US-0450072.
                                                                                                                                          represents
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Pred. No. 1.2
0; Mismatches
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Pred. No.
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                                                                                                                                          vaccae epitope
                                                                                                                                        The epitopes are especially useful of for producing vaccines. The case epitope of the invention.
                                                               DB 22;
1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.2e+02;
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                                                     Indels
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                                                                                                                                                                                                                                                                                               immune disorders
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is gastro-intestinal tract (GIT) transport receptor targeting agent, ZElan024. This peptide is capable of facilitating transport of an active agent e.g. a drug through gastro-intestinal tissue. The present sequence may be used as an immunogen, for the generation of antibodies which specifically bind to the present sequence.
                                               Secreted protein; human; treatment; diagnosis; therapy; cancer; tumour; neurodegenerative disorder; developmental abnormality; blood disorder; fetal deficiency; blood disorder; leukemia; immune system; inflammation; autoimmune disease; hepatic disease; renal disease; allergy; restenosis; ischaemic shock; Alzheiner's disease; cognitive disorder; schizophrenia; cardiovascular disorder; wound healing; stroke; arthritis; obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody specific to a domain of a gastrointestinal (GIT) agent such as ZElan033, ZElan088 and ZElan053, useful for quantitating and locating GIT targeting agents - \,
                          metabolic disorder.
                                                                                                                                       Human secreted protein fragment encoded from gene 12.
                                                                                                                                                                    04-OCT-1999
                                                                                                                                                                                                                    AAY25795 standard;
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         detecting,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-451689/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O'Mahony DJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       targeting agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gastro-intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gastro-intestinal tract transport receptor targeting agent ZElan024
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                                                                                                                                                                                                                                                                                  38 hpgg 41
                                                                                                                                                                                                                                                                                                 1 HPGG 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                          19, quantitating and locating the GIT transport receptor targeting
                                                                                                                                                                                                                                                                                                                                                                                                      41
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                                                                                                                                                                                                                                                                                                                                     100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody generation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 pp;
                                                                                                                                                                                                                    Protein; 42
                                     psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                 Score 27; Pred. No.
                                                                                                                                                                                                                                                                                                                                       Mismatches
                                     transplant
                                                                                                                                                                                                                                                                                                                                                 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                               DB
                                     rejection;
                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                              Length 41;
                                    infection;
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                                                                                                                                                                                                                       AAG27100
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Best Local
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30-JAN-1998;
30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  medical conditions e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 67 polynucleotides of the invention, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and fetal deficiencies, blood disorders, leukemias, disease, inflammation, altergies, ischaemic shock, Alzhaimer's and renal disease, inflammation, altergies, ischaemic shock, Alzhaimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           secreted proteins (see AAY25711-Y25778) and fragments (see AAY25779-Y25907) they encode. The polynucleotides and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating
                                              Zea mays protein fragment SEQ
                                                                                                17-OCT-2000
                                                                                                                                                 AAG27100
                                                                                                                                                                                          AAG27100 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders, wound healing, stroke, arthritis, obesity, asthma, acne, psoriasis, transplant rejection, metabolic disorders, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 348-349; 393pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated human genes and the secreted useful in, e.g. treatment of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-469315/39.
N-PSDB; AAZ00421.
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                                                                                                                                                                                                                                                                                                                    hpgg
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98US-0073165.
98US-0073167.
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98US-0073160.
98US-0073161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            describes novel human genes (see AAZ00410-Z00477) and the ns (see AAY25711-Y25778) and fragments (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0073162
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 27; DB 20; L
Pred. No. 1.3e+02;
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                                              ID
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                                              NO:
                                                 31806.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 42;
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Search completed: August 9, 2001, 20:24:14 Job time: 248 sec
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Pred. No. 1.3e+02;
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US-08-586-772-80
US-08-959-512-80
US-08-951-767a-63
US-08-951-767a-63
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US-08-801-972-5
US-08-801-972-4
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Patent No. 5217869
Sequence 80, Appl
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Sequence 63, Appl
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Sequence 339, App
Sequence 339, App
Sequence 368, App
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Sequence 4, Appli
Sequence 8, Appli
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RESULT 2 US-08-811-028-52 US-08-811-028-52 US-08-811-028-52 Sequence 52, Application US/08811028C Patent No. 5891671 GENERAL INFORMATION: APPLICANT: SUZUKI, Yuli APPLICANT: MASUDA, Toyofumi TITLE OF INVENTION: METHOD FOR CLEAVING CHIMERIC ENZYME USING PROCESSING TITLE OF INVENTION: ENZYME FILLE REFERENCE: 001560-294 CURRENT APPLICATION NUMBER: US/08/811,028C CURRENT FILLNG DATE: 1987-03-04 EARLIER FILLNG DATE: 1996-03-04 UNUMBER OF SEQ ID NOS: 54 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 52 LENGTH: 15 TYPE: PRI ORGANISM: Artificial Sequence FEATURE OTHER INFORMATION: Description of Artificial Sequence:modified OTHER INFORMATION: Lew, ile, ser, thr, asp, glu, asn, gln, lys, arg,	Query Match 100.0%; Score 27; DB 6; Length 5; Best Local Similarity 100.0%; Pred. No. 1.5e+05; Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps Qy 1 HPGG 4	RESULT 1 5217869-67 ; Patent No. 5217869 ; APPLICANT: KAUVAR, LAWRENCE M. ; APPLICANT: KAUVAR, LAWRENCE M. ; APPLICANT: KAUVAR, LAWRENCE M. ; REAGENTS ; NUMBER OF SEQUENCES: 121 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/07/255,906 ; EILING DATE: 11-OCT-1988 ; SEQ ID NO:67: ; LENGTH: 5 5217869-67	8 27 100.0 457 2 US-08-833-610-4 Sequence 4, Appl 9 27 100.0 457 3 US-08-834-033A-2 Sequence 2, Appl 0 27 100.0 457 3 US-08-834-033A-14 Sequence 14, Appl 1 27 100.0 457 4 US-09-363-574-2 Sequence 14, Appl 2 27 100.0 508 2 US-08-861-464-10 Sequence 10, Appl 3 27 100.0 508 2 US-08-96-001-10 Sequence 10, Appl 2 100.0 508 4 US-09-323-433A-10 Sequence 10, Appl 2 27 100.0 508 4 US-08-742-273-2 Sequence 2, Appl 3 27 100.0 510 1 US-08-742-273-2 Sequence 2, Appl 3 27 100.0 510 1 US-08-742-273-2	28 27 100.0 440 1 US-07-930-686-12 Sequence 12, Appl 29 27 100.0 440 2 US-08-460-998-12 Sequence 2, Appl 30 27 100.0 446 2 US-08-833-610-2 Sequence 2, Appl 31 27 100.0 446 2 US-08-833-610-5 Sequence 5, Appl 32 27 100.0 446 3 US-08-834-033A-5 Sequence 5, Appl 32 27 100.0 446 3 US-08-834-033A-15 Sequence 5, Appl 33 27 100.0 448 1 US-08-366-779-5 Sequence 5, Appl 35 27 100.0 448 1 US-08-366-779-5 Sequence 5, Appl 36 27 100.0 455 1 US-08-035-928-2 Sequence 2, Appl 37 27 100.0 457 2 US-08-834-655-2 Sequence 2, Appl 37 27 100.0 457 2 US-08-834-655-2 Sequence 2, Appl 37 27 100.0 457 2 US-08-834-655-2 Sequence 2, Appl 37 27 100.0 457 2 US-08-834-655-2 Sequence 2, Appl 37 27 100.0 457 2 US-08-834-655-2 Sequence 2, Appl 37 28 28 28 28 28 28 28 28 28 28 28 28 28
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Best Local S
Matches 4
                                                          Sequence 80, Application US/08586772 Patent No. 5874239
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                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/383,753
FILING DATE: 03-FEB-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,991
FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1
              APPLICANT: Schatz, Peter J. TITLE OF INVENTION: Biotiny
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STATE: California
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Schatz, Peter J.
TITLE OF INVENTION: Biotinylation of Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 103
                                                                                                                                                          19 HPGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER: US/08/383,753
03-FEB-1995
                                                                                                                                                                                                                                                                                                                peptide
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           Biotinylation of Proteins
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; MOLECULE TYPE:
US-08-586-772-80
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 80, Appli
Patent No. 5932433
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Best Local Similarity
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              FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/383,753
FILING DATE: 03-FEB-1995
                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rel-Base #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Schatz, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 HPGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 30-JUI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: One Market | CITY: San Francisco
                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                 ZIP:
                                                                                                                                                                                                                                                COUNTRY:
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APPLICATION NUMBER:
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30-JUL-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide
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us 08/099,991
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; MOLECULE TYPE: US-08-751-767A-63
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             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 63,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                           TELEPHONE: 7038164091
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: line
                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 415-326-2400
                                                                                                                                                           SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 30-JUL-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: V
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REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1038.1
                                                                                                              TYPE: amino acid TOPOLOGY: linear
                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                            40 amino acids
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1100 NORTH GLEBE ROAD
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100.0%; Score 27; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
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Pred. No.
                                                                                                                                                                                                                                          17-221
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Mismatches
                              DB 2; Length 40;
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COUNTRY: United .....

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/851,843A

TT.TNG DATE: 06-MAY-1997
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US-09-188-930-131
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APPLICANT: Watson, James D.
APPLICANT: Strechlan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
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Best Local Similarity
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LENGTH: 70
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SOFTWARE: FastSEQ for Windows Version 3.0
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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CITY: San Francisco
STATE: California
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Chapman, Karen B.
Morin, Gregg B.
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100.0%; Pred. No.
tive 0; Mismatch
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FILING DATE:

APPLICATION NUMBER: US 08/844,419

18-APR-1997

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US-08-974-549A-339
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Best Local Similarity
Watches 4; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 220:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION UNATA:
APPLICATION UNBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                 CLASSIFICATION: 536
PRIOR APPLICATION UNDATA:
APPLICATION UNDBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                          APPLICATION NUMBER: US/08/974,549A FILING DATE: 19-NOV-1997
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                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
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VENTION: Human Telomerase Catalytic Subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
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Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 4; Conser
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                                                                 COUNTRY: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
SOFTWARE: WOLD
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Edwards, Jean-Baptiste D. APPLICANT: Duelert, Aymeric APPLICANT: Lacroix, Bruno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,4;
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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TELEPHONE: (415) 576-0200
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APPLICATION NUMBER: 1
ATTORNEY/AGENT INFORMATION:
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               APPLICATION NUMBER: US/08/905,223 FILING DATE: CLASSIFICATION: 536
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                                                                                                                                                                                                                    CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 HPGG 78
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14-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: :
                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                NAME: Billings, Lucy J. 749
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/80 FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: PROTEIN ORIGINAL SOURCE: ORGANISM: Homo Sapiens
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LENGTH: 97 amino acids
TYPE: AMINO ACID
                                          SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acid
                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3174 POR CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Wil
                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304
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OTHER INFORMATION:
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IDENTIFICATION METHOD: Von Heijne matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE TYPE: Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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               STRANDEDNESS:
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LOCATION: -21..-1
TOPOLOGY:
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REGISTRATION NUMBER:
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                        : 104 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                      E: Incyte Pharmaceuticals, Inc
3174 Porter Drive
                                                                                     415-845-4166
                                                                                                                                                                                                                                                                                                                                                                          USA
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linear
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              single
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N: A NOVEL HUMAN CYTOCHROME
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29,655
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US-09-178-881-5
; Sequence 5, Application US/09178881
; Patent No. 6083704
; GENERAL INFORMATION:
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; LIBRARY: GenBank
; CLONE: 1217655
US-08-801-972-5
RESULT 13
US-08-801-972-4
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US-09-178-881-5
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Best Local Similarity
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Best Local Similarity
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MEDIUM TYPE: Diskett
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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CITY: Palo Alto
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LIBRARY: GELL
TONE: 1217655
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                                                     13 HPGG
                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                               NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/178,881
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                                                                               1 HPGG 4
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                                                     16
                                                                                                                                                                                                                                                                     104 amino acids
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N: A NOVEL HUMAN CYTOCHROME B5
                                                                                                                      100.0%;
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                                                                                                                      Score 27; DB 3;
Pred. No. 1.2e+02;
                                                                                                         Mismatches
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Sequence 4, Application US/08801972 Patent No. 5831018

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ENERAL INFORMATION:

Surya K.

FILING DATE:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local :
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NFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linea
IMMEDIATE SOURCE:
LIBRARY: GenBan
CLONE: 476415
          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                 STREET: 31.
CITY: Palo Alto
TWATE: CA
TWATE: TISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                              APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOV
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOUTO Bhort
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskette
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SOFTWARE: FastSE(
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CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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APPLICATION NUMBER:
                                                                                                                                                                                  ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
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                                                                                                                   94304
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Best Local Similarity
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                                              TELEPHONE: (416) 364-73
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO:
                                                                                                                                     APPLICATION NUMBER: US/09,
FILING DATE: 13-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy
                              SEQUENCE CHARACTERISTICS:
                                                                                       REFERENCE/DOCKET NUMBER: 65
TELECOMMUNICATION INFORMATION:
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LENGTH: 134 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                 LENGTH:
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            134 amino acids
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VENTION: Method of Determining Predisposition
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MOLECULE TYPE: Peptide

ORGANISM: POTCINE Cytochrome b5

US-09-041-517-1

Ouery Match
Best Local Similarity 100.0%; Score 27; DB 3; Length 134;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
MATCHES 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 44 HPGG 47

Search completed; August 9, 2001, 20:25:06

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Perfect score:
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       9, 2001, 20:26:03 ; Search time 50.69 Seconds (without alignments) 6.011 Million cell updates/sec
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31 4 A; Note: sequence

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Query Match
Best Local Similarity
Matches 4; Conserv

100.0%; Score 27; DB 2; Length 38; ilarity 100.0%; Pred. No. 51; Conservative 0; Mismatches 0; Indels

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Ouery Match Best Local Similarity 100.0%; Pred. No. 23; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 HPGG 4 Db 6 HPGG 9 RESULT 2 A48158 pheromone precursor MF alpha - fungus (Filobasidium floriforme) C. Species: Filobasidiella neoformans, Cryptococcus neoformans C. Date: 16-reb-1994 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994 C. Accession: A48158 R. Moore, T.D.; Edman, J.C. Mol. Cell. Biol. 13, 1962-1970, 1993 A. Filte: The alpha-mating type locus of Cryptococcus neoformans contains a peptide ph A. Reference number: A48158; MUID:93180845 A. Accession: A48158 A. Status: preliminary A. Molecule type: nucleic acid A. Residues: 1-38 CMOOP A. Note: sequence inconsistent with nucleotide translation A. Note: Sequence inconsistent with nucleotide translation A. Note: Sequence corrected from ACESTAL ACCESTAL ACCESTAL A. Note: Sequence inconsistent with nucleotide translation A. Note: Sequence inconsistent with nucleotide translation	RESULT 1 151879 1751879 cystathionine beta-synthase - human (fragment) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000 C;Accession: I51879 R;Sebastio, G.; Sperandeo, M.P.; Panico, M.; de Franchis, R.; Kraus, J.P.; Andria, G. Am. J. Hum. Genet. 56, 1324-1333, 1995 A;Title: The molecular basis of homocystinuria due to cystathionine beta-synthase def A;Reference number: I51879; MUID:95282779 A;Accession: I51879 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-16 <res> A;Cross-references: GB:S78267; NID:g999349; PIDN:AAB34404.1; PID:g999350</res>	30 27 100.0 120 2 \$63052 31 27 100.0 121 2 H96631 32 27 100.0 124 2 T40071 33 27 100.0 124 2 S20784 34 27 100.0 127 2 T37112 35 27 100.0 129 2 T41083 36 27 100.0 129 2 T36299 36 27 100.0 129 2 T36299 37 27 100.0 132 2 E84905 38 27 100.0 132 1 CBHO5 39 27 100.0 134 1 CBRB5 40 27 100.0 134 1 CBBB5 41 27 100.0 134 1 CBBB5 42 27 100.0 134 1 CBBC5 43 27 100.0 134 1 CBBC5 43 27 100.0 134 1 CBBC5 44 27 100.0 134 1 CBBC5 45 27 100.0 134 2 T52469 45 27 100.0 134 2 T14454 ALIGNMENTS	
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A;Cross-references: GB:S61885; NID:g237968; PIDN:AAB20155.1; PID:g237969
C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductive c;Keywords: chromoprotein; dimer; electron transfer; FAD; flavoprotein; heme; iron; meta fr:7:744Domain: cytochrome b5 core homology (fragment) <CB5>
                                                                                                                                         nitrate reductase (NADH) (EC 1.6.6.1) - curled-leaved tobacco (fragment) c;Species: Nicotiana plumbaginifolia (curled-leaved tobacco) C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 11-Jun-1999 C;Accession: A41085 R;Meyer, C.; Levin, J.M.; Roussel, J.M.; Rouze, P. J. Biol. Chem. 266, 20561-20566, 1991 A;Ritle: Mutational and structural analysis of the nitrate reductase heme da A;Reference number: A41085; MUID:92041899 A;Accession: A41085; MUID:92041899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: root, cv. Naehan C; Superfamily: cytochrome b5; cytochrome F;1-51/Domain: cytochrome b5 core homoly
                                                                                     A; Molecule type: mRNA
A; Residues: 1-74 <MEY>
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Plant Sci. 133, 191-201, 1998
A;Title: Analysis of randomly selcelted cDNAs reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein - barley (fragment)
C:Species: Hordeum vulgare (barley)
C:Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change
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A;Title: Generation of expressed sequence A;Reference number: PQ0816; MUID:94302145
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C; Date: 03-May-1994
C; Accession: PQ0816
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A; Accession: T05913
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A; Residues: 1-51 <PAR>
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Best Local Similarity

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be: cv. Haisa, leaf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 27;
Pred. No.
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82;
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ment) <CB5>
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R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V; Ber C; Bron, S, Brouillet, S, Bruschi, C.V.; Caldwell, B.; Capuano, V; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A; A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A; A; A; Carter, M.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Carter, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galizzi, Galizzi, A.; Galizzi, A.; Galizzi, A.; Galizzi, A.; Galizzi, Galizzi, A.; Galizzi, A.; Galizzi, A.; Galizzi, A.; Galizzi, A.; Galizzi, A.; Galizzi, A.; Galizzi, A.; Galizzi, A.; Galizzi, A.; Galizzi, A.; Galizzi, A.; Galizzi, A.; Galizzi, A.; Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi, Galizzi
                                                                                                                                                                                                                                                                               C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000 C;Accession: S76591 R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; 10, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada DNA Res. 3, 109-136, 1996
A; Molecule type: DNA
A; Residues: 1-79 <KAN>
A; Cross-references: EMF
A; Note: the nucleotide
                                                                                                                                                             A; Reference number: S74322; MUID: 97061201 A; Accession: S76591
                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Synechocystis sp. A;Variety: PCC 6803
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C;Superfamily: conserved hypothetical protein HI1000
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A; Residues: 1-75 < KUN>
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                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                         A; Title:
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Best Local S
Matches 4
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ce: strain 1
                                     EMBL: D64002;
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      GB:AB001339;
was submitted
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Pred. No.
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Pred. No.
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      NID:g1001612;
to the EMBL Da
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                                     PIDN:BAA10437.1;
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sequence

Data

C;Superfamily:

conserved

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$07959 cytochrome b5, microsomal splice form N;Alternate names: hepatic cytochrome
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                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-86 <STO>
                                                                                                                                                                                                                                                                                                                                                                   A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path A;Reference number: A82950; MUID:20437337 A;Accession: D83389
                                                                                                                                                                                                                                                                                                                                                                                                                    R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, F.; LOTY, S.; Olson, M.V.; Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein PA2045 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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R;Lammers, R.; Gross, G.; Mayr, U.; Collins, Eur. J. Biochem. 178, 93-99, 1988
A;Title: Alternative mechanisms for gene act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9K protein (clone pG4) - human
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change
                                                                                                                                                                                                                                            C; Superfamily: conserved
                                                                                                                                                                                                                                                              A; Gene: PA2045
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                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
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A; Residues: 1-82 <LAM>
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Pred. No.
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Pred. No.
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                     brown howler monkey (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Warrener, P.;
K.R.; Kas, A.;
                                                                                                                                                                                                                                                                                                        PIDN: AAG05433.1;
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RESULT 12
I40653
9K protein - 0
C;Accession: I40653
R;Suhan, M.; Chen, S.Y.; Thompson, H.A.; Hoover, T.A.;
J. Bacteriol. 176, 5233-5243, 1994
A;Title: Cloning and characterization of an autonomous
A;Reference number: I40647; MUID:94350801
A;Accession: I40653
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: T04413
R;Lee, J.E.; Parthier, B.; Loebler, submitted to the EMBL Data Library, A;Description: Jasmonate signalling A;Reference number: Z15346
A;Accession: T04413
                                                                                                                                                            C;Species: Coxiella burnetii
C;Date: 12-Aug-1996 *sequence_revision 12-Aug-1996 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable naringenin-chalcone synthase (EC 2.3.1.74) - barley (fragment)
C;Speckes: Hordeum vulgare (barley)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C;Accession: T04413
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A; Molecule type: protein
A; Residues: 1-10, 'Q', 12-13, 'E', 15-57, 'D', 59-74, 'Y', 76-84, 'K', 86, 'R' <NO
C; Superfamily: cytochrome b5; cytochrome b5 core homology
C; Keywords: electron transfer; heme; iron; liver; metalloprotein
E; 5-80/Domain: cytochrome b5 core homology <CB5>
F; 40, 64/Binding site: heme iron (His) (axial ligands) #status predicted
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C; Keywords:
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A;Residues: 1-87 <0205
R;Nobrega, F.G.; Ozols, J.
J. Biol. Chem. 246, 1706-1717, 1971
J. Biol. Chem. 246, 1706-1717, 1971
A;Title: Amino acid sequences of tryptic peptides of cytochromes b-5 from microsomes A;Reference number: 92077; MUID:71134790
A;Accession: A92077
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C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-May-2000
C;Accession: S07959; A92077; A00167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: cv. Salome, leaf C; Superfamily: chalcone synthase
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A; Residues: 1-87 <LEE>
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Pred. No. 1.1e+02;
; Mismatches 0;
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A; Experimental : C; Genetics: A; Gene: Rv0942
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A; Residues: 1-97 <WIE>
C; Superfamily: chalcone synthase
                                                                                                                                                                                                                                                      A;Title: Structural organization and differential expression of three stilbene synthase A;Reference number: S53313; MUID:95036047 A;Accession: S53315
                                                                                                                                                                                                                                                                                                                                          stilbene synthase - grape
C;Species: Vitis sp. (grape)
C;Date: 14-Jul-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C;Accession: S53315
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A:Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
A;Accession: D70715
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
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A;Residues: 1-88 <RES>
A;Cross-references: EMBL:U10529; NID:g511451; PIDN:AAA56918.1; PID:g511458
C;Superfamily: conserved hypothetical protein HI1000
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein Rv0942 - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Decies: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999 C;Accession: D70715
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A; Residues: 1-92 <COL>
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Pred. No. 1.1e+02;
                                                                                             Score 27; DB 2;
Pred. No. 1.2e+02;
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Pred. No. 1.1e+02;
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Job time: 243 sec
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2001, 20:26:04

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A;Note: a deficiency of this protein causes type IV hereditary methemoglobinemia C;Superfamily: cytochrome b5; cytochrome b5 core homology C;Keywords: acetylated amino end; alternative splicing; chromoprotein; electron trans F;2-98/Product: cytochrome b5, erythrocyte splice form #status experimental <MAT> F;9-84/Domain: cytochrome b5 core homology <CB5> F;2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental F;44,68/Binding site: heme iron (His) (axial ligands) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytochrome b5, erythrocyte splice form [validated] - C;Species: Homo saptens (man) C;Date: 08-Aug-1987 #sequence_revision 05-Apr-1995 #t C;Accession: JN0075; B24211
В
                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: GDB:CYB5
A;Cross-references: GDB:125236; OMIM:250790
A;Map position: 18q23-18q23
A;Introns: 86/3
A;Introns: 86/3
A;Note: the list of introns may be incomplete
C;Function:
C;Function:
A;Description: acts to reduce methemoglobin to functional hemoglobin; the oxidized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: erythrocyte C; Comment: Cytochrome b5 exists in at least two C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M60174; NID:g181391; A;Experimental source: erythrocyte R;Abe, K.; Kimura, S.; Kizawa, R.; Anan, F.K J. Biochem. 97, 1659-1668, 1985
A;Title: Amino acid sequences of cytochrome A;Reference number: A91992; MUID:85289161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Giordano, S.J.; Steggles, A.W.
Biochem. Biophys. Res. Commun. 178, 38-44, 1991
A;Title: The human liver and reticulocyte cytochrome
A;Reference number: JN0075; MUID:91298976
A;Accession: JN0075
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A; Residues: 2-88, 'K', 90, 'R', 92-98 <ABE>
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A; Residues: 1-98 <GIO>
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Pred. No. 1.2e+02;
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Copyright (c) 1993 - 2000 Compugen
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ALIGNMENTS

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                        EMBL; X13956; CAA32138.1; PIR; S02660; S02660.
                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90256715; pubMed-2341375;
Kumazaki T., Hoshiba N., Yokosawa H., Ishii S.-I.;
"Primary structure of ascidian trypsin inhibitors in the hemolymph of
a solitary ascidian, Halocynthia roretzi.";
  SEQUENCE
                                                                                                                                                                                                                                                                             "Alternative mechanisms for gene activation induced by poly(rI), poly(rC) and Newcastle disease virus.";
Eur. J. Biochem. 178:93-99(1988).
-i- INDUCTION: BY POLY(RI), POLY(RC) AND NEWCASTLE DISEASE VIRUS.
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MEDLINE=90256716; PubMed=2111316;
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Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-89078418; PubMed-3203696;
Lammers R., Gross G., Mayr U., Collins J.;
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MEDLINE-90256715;
                                                                                                                                                                                                                 between
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4121548DB33207C2 CRC64;
  9B4A15552A489652 CRC64;
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Pred. No.
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RESULT 5
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                    Alouatta seniculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                 CYTOCHROME B5 (FRAGMENT).
                                                                            21-JUL-1986 (Rel.
01-OCT-1989 (Rel.
01-OCT-2000 (Rel.
                                                                                                              CYB5_ALOSE
P00168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hansen F.G., Hansen E.B., Atlung T.; "Physical mapping and nucleotide sequence of the rnpA gene that encodes the protein component of ribonuclease P in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
Bacteria; Proteobacteria;
Escherichia.
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01-AUG-1991 (Rel. 19, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 9.4 KDA PROTEIN IN RNPA-THDF INTERGENIC REGION
                                                                                                                                                                                                                                                                                       Hypothetical protein SEQUENCE 85 AA; 9:
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NCBI_TaxID=9503
          Alouatta.
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EG11348; YidD.
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PIR; A00167; CBHU5.
PIR; S07959; S07959.
HSSP; P00171; 3B5C.
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Nobrega F.G., Ozols J.;
Namino acid sequences of tryptic peptides
"Amino acid sequences of tryptic peptides
microsomes of human, monkey, porcine, and
microsomes of human, monkey, porcine, and
microsomes of human, 246:1706-1717(1971).
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                                                                           Williams J.C.;
"Cloning and characterization of an from Coxiella burnetil.";
J. Bacteriol. 176:5233-5243(1994).
                                                                                                                         STRAIN-NINE MILE PHASE I / BRATISLAVA; MEDLINE-94350801; Pubmed-8071197; Suhan M., Chen S.Y., Thompson H.A., Ho
                                                                                                                                                                                  Bacteria; Proteobacteria;
Coxiella group; Coxiella.
NCBI_TaxID=777;
                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
HYPOTHETICAL 9.9 KDA PROTEIN IN RNPA 3'REGION
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PROSITE; PS00191; CYTOCHROME_B5_1; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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SEQUENCE.
MEDLINE=71134790; PubMed=4993957.
                                                                                                                                                               SEQUENCE FROM
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PubMed=2752049;
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HEME LIGAND (BY SIMILARITY).
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RPK -> KPR (IN REF. 1).
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chicken liver.";
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RESULT 7
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"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
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Hypothetical protein.
SEQUENCE 88 AA; 9923
                                                                                                                                                                                                                  Hypothetical
SEQUENCE 9
                                                                                                                                                                                                                                                               EMBL; Z79700; CAB01979.1; TubercuList; Rv0942; -.
                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98295987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actinomycetales;
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RV0942 OR MTCY10D7.32C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U10529; AAA56918.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
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  66
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HPGG
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  69
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                                                                                                                                                                                                                  92 AA;
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L 9.7 K
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llarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterineae;
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                                                                                                                                                                                                                  9737 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9923 MW;
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                                                                                            Score 27; DE
Pred. No. 56;
0; Mismatches
                                                                                                                                                                                                                  F0732A4A607D47C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 27; Pred. No.
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Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                              (See
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                                                                                                                   56;
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MBL outstation -
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RESULT 8
CHSY_FRAAN

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Best Local Similarity
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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ADULT-SPECIFIC RIGID CUTICULAR PROTEIN 11.9 (ACP 11.9).
Araneus diadematus (Spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Araneoidea; Araneidae; Araneus.
NCBI_TaxID-45920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; irnve
Pfam; PF00195;
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01-OCT-1996
15-JUL-1999
                                                                                                                                                                                         P80515;
01-FEB-1996
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                                                                                                                                                                                                                                                                         ARADI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Mol. Biol. 27:1097-1108(1995).

-i- FUNCTION: THE PRIMARY PRODUCT OF THIS ENZYME IS 4,2',4',6'-
TETRAHYDROXYCHALCONE (ALECONE NARINGENIN-CHALCONE OR CHALCONE)

TETRAHYDROXYCHALCONE (ALECONE NARINGENIN-CHALCONE OR CHALCONE)

TETRAHYDROXYCHALCONE (ALECONE NARINGENIN-CHALCONE OR CHALCONE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilkinson J.Q., Lanahan M.B., Conner T.W., Klee H.J., "Identification of mRNAs with enhanced expression in strawberry fruit using polymerase chain reaction diff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Embryophy
Magnoliophyta; eudicotyledons; core
Rosales; Rosaceae; Fragaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Flavonoid biosynthesis; Transferase; NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U19942; AAA79923.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95284359; PubMed=7766892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CV.
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                                                                                                                                                                                                                                                                                                                                                                            13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: PART OF THE BIOSYNTHETIC PATHWAY FOR AL FLAVONOIDS, A LARGE CLASS OF SECONDARY PLANT MET OF WHICH ARE BRIGHTLY COLORED.
TISSUE SPECIFICITY: PREDOMINANTLY IN DEVELOPING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: 3 MALONYL-COA + 4-COUMAROYL-COA = 4 COA NARINGENIN-CHALCONE + 3 CO(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENTAL STAGE: EXPRESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NARINGENIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WHICH CAN UNDER SPECIFIC CONDITIONS
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PS00441; CHALCONE_SYNTH; PARTIAL
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(Rel. 34, Last sequence update)
(Rel. 38, Last annotation update)
NTHASE RJ5 (EC 2.3.1.74) (NARINGENIN-CHALCONE SYNTHASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Pred. No.
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RESULT 10
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Best Local
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SEQUENCE
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P40312;
01-FEB-1995 (Rel. 31, Created)
01-OCT-1996 (Rel. 34, Last seq
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                        This
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Pallavicini A., Lanfranchi G., Valle G.;
"The DNA sequence of cosmid 14-13b from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         which suppresses ketoconazole reductase-deficient strain."; Gene 142:123-127(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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-!- FUNCTION: COMPONENT OF THE RIGID CUTICLE OF THE SPIDER -!- MASS SPECTROMETRY: MW-11872.1; METHOD-ELECTROSPRAY.
                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae reveals an unusually high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Truan G., Epinat J.-C., Rougeulle C., Cullin C., Pom
"Cloning and characterization of a yeast cytochrome
which suppresses ketoconazole hypersensitivity in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYB5 OR YNL111C OR N1949.
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HSSP; P04002; latf.
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SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BI SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
SWISS-PROT entry is copyright.
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EMBL; Z69382; CAA93396.1; -
EMBL; Z71387; CAA95990.1; -
PIR; S47919; S47919.
HSSP; P04166; 1B5M.
SGD; S0005055; CYB5.
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BINDING 61
TRANSMEM 98 1
CONFLICT 17
                                                                 entities
or send a
                                                                                                                                                                                                                                                                 delta6-desaturated fatty acids in transgenic tobacco.";
Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216 (1997).
-i- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTE FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE OXYGENASES (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO T CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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PROSITE; PS50255; CYTOCHROME_B5_2; 1.
Electron transport; Transmembrane; Heme;
BINDING 37 37
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CONFLICT 17 17 E -> Q (IN 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sayanova O., Smith M.A., Lapinskas P.A., Stobart K. Christie W.W., Shewry P.R., Napier J.A.; "Expression of a borage desaturase cDNA containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000
01-OCT-2000
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                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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an email to license@isb-sib.ch).
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CYB5_BOVIN

STANDARD;

p00171; Q28837; Q27947;

21_JUL_1986 (Rel. 01, Crr

01_JUL_1989 (Rel. 11, Lax

01-OCT-2000 (Rel. 40, La;

CYTOCHROME B5.
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SEQUENCE
                                                                                                                                                                       MEDIINE-85389161; PubMed-4030743;
Abb K., Kimura S., Kizawa R., Anan F.K., Sugita Y.;
"Amino acid sequences of cytochrome b5 from human, porcin bovine erythrocytes and comparison with liver microsomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYB5
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Bovinae; Bos.
                                                        "Cytochrome b5 from microsomal membranes porcine livers. Isolation and properties the membranous segment.";
Biochemistry 13:426-434(1974).
                                                                                                        Ozols J
                                                                                                                                                                                                                                                                 and a transcribed pseudogene."; Genomics 17:348-354(1993).
                                                                                                                                                                                                                                                                                                             TISSUE=Liver;
MEDLINE=94010928; PubMed=8406485;
                                                                                                                                                                                                                                                                                                                                                               Nucleic
                                                                                                                                                                                                                                                                                                                                                                             mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-89128451; Pubmed-
Cristiano R.J., Steggles
                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9913;
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Pfam; PF00173; heme_1; 1
           Ozols J.,
                     SEQUENCE OF 5-96. • MEDLINE=70067001; PubMed=5391285;
                                                                                                                   MEDLINE=74080219;
                                                                                                                                SEQUENCE OF 1-10 AND 130-133.
                                                                                                                                                                                                                             TISSUE-Erythrocyte;
                                                                                                                                                                                                                                          SEQUENCE OF 1-97
                                                                                                                                                                                                                                                                                         "The isolation and characterization of
                                                                                                                                                                                                                                                                                                 Cristiano R.J., Giordano S.J., Steggles A.W.;
                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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PSO0191, CYTCCHROME_B5_2; 1.

PS50255; CYTOCHROME_B5_2; 1.

Transport; Transmembrane; Heme; Microsome.

Transport; Transmembrane; Heme; Microsome.

HEME LIGAND (BY SIMILARITY).

61 61 HEME LIGAND (BY SIMILARITY).

M 104 124 POTENTIAL.

M 104 124 POTENTIAL.

F 132 AA; 14556 MW; 96EF72A06F2EBC5B CRC64;
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            Strittmatter
                                                                                                                                                       97:1659-1668(1985).
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the amino acid sequence of calf liver microsomal
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124
14556 MW;
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                                                                                                                     PubMed=4810060;
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EMBL; M63326; AAC1445:
EMBL; M63327; AAC1445:
EMBL; L22966; -; NOT_J
PIR; A00170; CBB05.
PIR; F24211; F24211.
PIR; S03428; S03428.
PIR; S07963; S07963.
                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
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MEDLLNE-70289989; PubMed=5272324;

MEDLLNE-70289989; PubMed=5272324;

Tsugita A., Kobayashi M., Tani S., Kyo S., Rashid M.A., Yoshid Tsugita A., Hagihara B.;

"Comparative study of the primary structures of cytochrome b5 four species.";

Tour species.";
                                                                                                                                                                                                                                                                                                          J. MOI. BIOL. 258:172-189(1996).
J. MOI. BIOL. 258:172-189(1996).
J. FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Argos P., Mathews F.S.;
"The structure of ferrocytochrome b5
J. Biol. Chem. 250:747-751(1975).
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MEDLINE=89323209; PubMed=2752049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=78218214; PubMed=670203; Fleming P.J., Dailey H.A., Corcoran D., The primary structure of the nonpolar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 2
                                                                                                                                                                                                                                                                                                                                                              Muskett F.W., Kelly G.P., Whitford D.;
"The solution structure of bovine ferricytochrome
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"The structure of cy
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                                                                                                                                                                       European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM. SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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Spring Harb.
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                                                          AAC14455.1; ALT_SEQ.
AAC14455.1; JOINED.
AAC14455.1; JOINED.
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-; NOT_ANNOTATED_CDS.
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Pubmed=1167544;
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RESULT 13
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Best Local (
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DOOLS J., Gerard C., Nobrega F.G.;
OZOLS J., Gerard C., Nobrega F.G.;
"Proteolytic cleavage of horse liver
of the heme-containing moiety.";
J. Biol. Chem. 251:6767-6774(1976).
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Equus caballus (Horse).

Craniata; Vertebrata;

Craniata; Vertebrata;
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01-OCT-1989 (Rel.
01-OCT-2000 (Rel.
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SEQUENCE OF 89-133.
MEDLINE=78045981; PubMed=562879;
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                                                                         NCBI_TaxID=9796;
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InterPro; IPR001199; -
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HEME LIGAND (BY SIMILARITY).

AEES -> ZSZZBA (IN REF. 5).

EIQ -> QIE (IN REF. 5).

N -> D (IN REF. 5 AND 6).

S -> SES (IN REF. 2).

N -> D (IN REF. 4).
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Pred. No.
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RESULT 14
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01-OCT-2000
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Li X.R., Giordano S.J.,
Submitted (MAR-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ozols J., Gerard C.;
"Covalent structure of the membranous segment of Chemical cleavage of the native hemoprotein.";
J. Biol. Chem. 252:8549-8553(1977).
       TISSUE-Erythrocyte;
MEDLINE-91298976; PubMed-1712589;
                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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PRINTS; PR00363; CYTOCHROMEB5
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MEDLINE=89323209; PubMed=2752049;
                           SEQUENCE OF 1-97 FROM
                                                                                    Biochem.
                                                                                            The complete nucleot
                                                                                                               TISSUE-Liver;
MEDLINE-89025904; PubMed-3178851;
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                                                                                                                                                                                Homo sapiens (Human)
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S07964; S07964.
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S.J.,
                                                                                   Biophys.
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CYTOCHROME B5 IS A MEMBRANE BOUND
AS AN ELECTRON CARRIER FOR SEVERAL
                                                                                             nucleotide
Steggles A.W.;
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                                                                                   Res.
                                                                                                                                                                                                         01, Created)
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                                                                                   Commun.
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the
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                                                                                  sequence of human liver
ommun. 156:576-580(1988)
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                                              M., Steggles A.W.
EMBL/GenBank/DDBJ
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HEME LIGAND (BY SIMILARITY).
AEQSD -> ZEDAS (IN REF. 1).
85E50818D8CF4247 CRC64;
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Pred.
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                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                      Mismatches
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PIR; A00167; PIR; A28936;

A28936. B24211. S04976.

L39944; AAA63169 M60174; AAA52165

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"Amino acid sequences of tryptic microsomes of human, monkey, porc
                                                                                                                                                                                                                                                        use by non-profit institutions as modified and this statement is not rementities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochim. Biophys. Acta 997:121-130(1989).
-!- FUNCTION: CYTOCHROME B5 IS A MEMBRANE
FUNCTION AS AN ELECTRON CARRIER FOR SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rashid M.A., Hagihara B., Kobayasi "Structural studies of cytochrome liver cytochrome b5.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abe
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MEDLINE=85289161; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-35 AMEDLINE-89323209;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             crosomes of human, monkey, porcine, Biol. Chem. 246:1706-1717(1971).
                                                                                                                                                                                                                                                                                                                                                                                        (SHOWN HERE) AND A ERYTHROCYTE/CYTOPLASMIC ALTERNATIVE SPLICING.
DISEASE: DEFECTS IN CYB5 ARE THE CAUSE OF TV METHEMOGLOBINEMIA.
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K., Kimura S., Kizawa R., Anan F.K., Sug
                                                                                                     .; M22865; AAA35729.1;

.; L39945; AAA63169.1;

.; L39979; AAA63169.1;

.; L39941; AAA63169.1;

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.; L39943; AAA63169.1;

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SUBCELLULAR LOCATION:
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a single gene."
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hem. 247:2242-2245(1972).
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B., Kobayashi M., T
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                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tani S., Tsugita A.;
Sequential studies
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                                                                                                                             MARITA M., Hiller L., Allen M., Bowles M., Dietrich N., Dubuque T.,
A Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,
A Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B.,
A Theising B., Wylle T., Lennon G., Soares B., Wilson R., Waterston R.;
A Theising B. Wylle T., Lennon G., Soares B., Wilson R., Waterston R.;
C -!- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
C -!- CUCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
C OXYGENASES. IT IS ALSO INVOLVED IN SEVERAL MEMBRANE BOUND
C OXYGENASES. IT IS ALSO INVOLVED IN THE C-5 DOUBLE BOND
C OXYGENASES. IT IS ALSO INVOLVED IN THE C-5 DOUBLE BOND
C INTRODUCTION DURING THE C-5 DESATURATION.
C -!- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
C CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
C -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CYTOCHROME B5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYB5_
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SEQUENCE
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MOD_RES
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DOMAIN
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VARSPLIC
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                      сүв5
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15-JUL-1998
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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PROSITE; PS50255; CYTOCHROME_B5_2;
Electron transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00173; heme_1; 1. PRINTS; PR00363; CYTOCHROMEB5.
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MIM; 250790; -.
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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MISSING (IN REF. 5).

Q -> E (IN REF. 8).

EEIQ -> QELE (IN REF. 5, 6 AND 7).

MISSING (IN REF. 7).

N -> D (IN REF. 7).

N -> D (IN REF. 8).

RPK -> KPR (IN REF. 4, 5, 6 AND 7).

A -> V (IN REF. 8).

MW: 2FAD2AEB7E6C992E CRC64;
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HEME-BINDING.
MEMBRANE-BINDING
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LIGAND (BY SIMILARITY).
P (IN ERYTHROCYTE ISOFO
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Matches 4
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PROSITE; PS50255; CYTOCHROME_B5_2; 1.
Electron transport; Transmembrane; Heme; Mi
INIT_MET 0 BY SIMILARITY

DOMAIN 1 90 HEME-BINDING
DOMAIN 91 133 MEMBE-BINDING
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EMBL; AA107511; -; NOT_ANNOTATED_CDS.
EMBL; AA086847; -; NOT_ANNOTATED_CDS.
EMBL; AA08541; -; NOT_ANNOTATED_CDS.
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SWISS-2DPAGE; P56395; MOUSE.
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                                                         43
                                                                                                                Local Similarity
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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RESULT 2 Q9UR51 ID Q9UR51 AC Q9UR51; PRELIMINARY; PRT; 22 AA. DT 01-MAY-2000 (TrEMBLrel. 13, Created) DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)	Query Match 100.0%; Score 27; DB 4; Length 16; Best Local Similarity 100.0%; Pred. No. 34; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 1 HPGG 4	RESULT 1 Q16350 Q16350 PRELIMINARY; PRT; DAA. AC Q16350; DT 01-NOV-1996 (TYEMBLTel. 01, Created) DT 01-NOV-1996 (TYEMBLTel. 01, Last sequence update) DT 01-NOV-1996 (TYEMBLTel. 08, Last annotation update) DT 01-NOV-1998 (TYEMBLTel. 08, Last annotation update) DC CYSTATHIONINE BETA-SYNTHASE (FRAGMENT). OS HOMO sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OX NCBI_TaxID=9606; RN [1] RN [1] RR MEDLINE=95282779; PubMed=776255; RX MEDLINE=95282779; PubMed=776255; RX MEDLINE=95282779; PubMed=776255; RA Andria G.; RA Andria G.; RA Andria G.; RA Andria G.; Sperandeo M.P., Panico M., de Franchis R., Kraus J.P., RA Andria G.; RA Andria G.; The molecular basis of homocystinuria due to cystathionine beta- RT synthase deficiency in Italian families, and report of four novel RT mutations."; RL Am. J. Hum. Genet. 56:1324-1333(1995). DR EMBL; S78267; AAB34404.1; FT NON_TER 1 1 SQ SEQUENCE 16 AA; 1538 MW; 07455C146B001686 CRC64;

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Garter D.A.;
"Presence of alpha and a mating types in collections of Cryptococcus neoformans ve
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EMBL;
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MEDLINE=99380307; PubMed=10449476;
Halliday C.L., Bui T., Krockenberger
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MEDLINE-99380307; PubMed=10449476;
Hall1day C.L., Bul T., Krockenberger M.,
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Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Tremellaceae; Filobasidiella.
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EMBL; AF155341; AAF19019.1;
EMBL; AF155340; AAF19018.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Tremellaceae; Filobasidiella
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                                                                                                                                                                                                                                                                                                                                                                                                                             collections of Cryptococcus neoformans
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L; AF155339; AAF19017.1; -.
L; AF155335; AAF19014.1; -.
L; AF155336; AAF19014.1; -.
L; AF155337; AAF19015.1; -.
L; AF155338; AAF19016.1; -.
L; AF155338; AAF19016.1; -.
SEPEC; IPRO00308; -.
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SEPEC; IPRO000600; -; 1.
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"A mitogenic peptide amide encoded within the E pept
"National Peptide amide encoded within the E pepting and the growth factor IB prohormone.";
Proc. Natl. Acad. Sci. U.S.A. 89:8107-8111(1992).
SEQUENCE 23 AA; 2508 MW; 40A5F3F520E3F789 CRC64;
                                                                                                                                                                                                                                               Mammuthus primigenius (Siberian woolly mammoth).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Proboscidea; Elephantidae; Mammuthus.
NCBI_TaxID=37349;
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Quinn K.A., Cuttitta F.;
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MEDLINE-92390398; PubMed-1325646;
MEDLINE-92390398; PubMed-1325646;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Eukaryota; Fungi; Basidiomycota;
Tremellaceae; Filobasidiella.
NCBI_TaxID=40410;
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Eukaryota; Metazoa; Chordata; Crar
Mammalla; Eutheria; Proboscidea; E
                                                                                                                                                 determine mating type, ploidy, and variety: and molecular pathogenesis studies.";
J. Clin. Microbiol. 38:2007-2009(2000).
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EMBL: AF155043; AAF12754.1; -
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PHEROMONE PRECURSOR MATALPHA
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J. Clin. Microbiol. 38:2007-2009(2000).
EMBL; AF226937; AAG41326.1; -.
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SEQUENCE 33 AA; 3430 MW; EE502A095DF450E
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Chaturvedi S., Roc
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                                                                                                                                                                                                                                                                                                                                                                                                                    Chaturvedi S., Rodeghier Chaturvedi V.;
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                                                                                                                 "Cryptococcus neoformans MAT-alpha pheromone sequence.", Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases EMBL, AF226889; AAG412781.; -. EMBL; AF214057; AAG41259.1; -. EMBL; AF214059; AAG41261.1; -. EMBL; AF214060; AAG41261.1; -. EMBL; AF214064; AAG41266.1; -.
                                                                                                                                                                                                                           determine mating type, ploidy, and variety:
and molecular pathogenesis studies.";
J. Clin. Microbiol. 38:2007-2009(2000).
                                                                                                                                                                                                                                                                                                                                  Filobasidiella neoformans var. neoformans. Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tremellaceae; Filobasidiella.
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Chaturvedi V.;
Submitted (JAN-2000)
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Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Trer
Tremellaceae; Filobasidiella.
NCBI_TaxID=5207;
                                                                                                                                                                                     Chaturvedi S., Rodeghier
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MAT-alpha pheromone
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01-MAR-2001 (TrEMBLrel. 16, I
PHEROMONE PRECURSOR MATALPHA
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                                                                               determine mating type, ploidy, and variety: and molecular pathogenesis studies."; J. Clin. Microbiol. 38:2007-2009(2000).
                                                                                                                                                                                                   STRAIN=VARIOUS STRAINS;
MEDLINE=20251028; PubMed=10790143;
Chaturvedi V.;
Chaturvedi V.;
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Eukaryota; Fungi; Basidiomycota;
Tremellaceae; Filobasidiella.
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STRAIN-VARIOUS STRAINS;
MEDLINE-20251028; PubMed-10790143;
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Eukaryota; Fungi; Basidiomycota;
Tremellaceae; Filobasidiella.
NCBI_TaxID=135857;
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  STRAIN-ATCC28957, UM3,
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AAG41277.1;

AAG41269.1;

AAG41270.1;

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AAG41276.1;
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MAT-alpha pheromone sequence.";
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Copyright (c) 1993 - 2000 Compugen
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ALIGNMENTS

RESULT AAW84144

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AAW84144;

AAW84144 standard; Peptide;

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malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis; cancer; diabetes; eczema; platelet aggregation; vasodilation; cholesterol level; endometriosis; premenstrual syndrome;
WPI; 1998-594582/50
                     Chaudhary S, Thurmond J;
                                                                                     11-APR-1997;
                                                                                                                                                      WO9846763-A1.
                                                                                                                                                                            Unidentified
                                                                                                                                                                                               myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis; acute respiratory syndrome; hypertension; inflammatory skin disorder.
                                                                                                                                                                                                                                                      Fatty acid; desaturase; polyunsaturated fatty acid;
                                                                                                                                                                                                                                                                          Desaturase enzyme peptide sequence.
                                                                                                                                                                                                                                                                                                  15-FEB-1999
                                                     (ABBO ) ABBOTT LAB.
(CALJ ) CALGENE LLC.
                                                                                                                                 22-OCT-1998
                                                                                                           10-APR-1998;
                                                                                                                                                                                                                                                                                                  (first entry)
                               Huang
                                                                                      97US-0834655
                                                                                                           98WO-US07126
                                 Y,
                                 Knutzon
                                 Ď,
                                  Leonard AE,
                                  Mukerji
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malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
cancer; diabetes; eczema; platelet aggregation; vasodilation;
cholesterol level; endometriosis; premenstrual syndrome;
myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
acute respiratory syndrome; hypertension; inflammatory skin disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used to inhibit platelet aggregation, cause vasodilation, lower cholesterol levels, inhibit proliferation of vessel wall smooth muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding and other side effects caused by non-steroidal anti-inflammatory drugs, prevent or treat endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis and chronic fatigue after viral infections, treat AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polyunsaturated fatty acids can be used for treating e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis, asthma, psorias cancer, diabetes or eczema or reduce blood pressure. They can also be used to inhibit platelet aggregation, cause vasodilation, lower
                                  WPI; 1998-594582/50
                                                                     Thurmond J;
                                                                                    Chaudhary S,
                                                                                                                                                                            11-APR-1997;
                                                                                                                                                                                                               10-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a peptide derived from a desaturase enzyme. The specification describes methods for desaturating a fatty acid and for producing a desaturated fatty acid by expressing fatty acid and for producing a desaturated fatty acid by expressing
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                                                                                                                     (ABBO ) ABBOTT LAB. (CALJ ) CALGENE LLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                    Huang
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Pred. No. 3.6e-06;
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                                                                                    Leonard AE,
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           after angioplasty, inflammation, rheumatoid arthritis, asthma, psoriasis, actor of diabetes or eczema or reduce blood pressure. They can also be used to inhibit platelet aggregation, cause vasodilation, lower cholesterol levels, inhibit proliferation of vessel wall smooth muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding and other side effects caused by non-steroidal anti-inflammatory drugs, prevent or treat endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis and chronic fatigue after viral infections, treat AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and
                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans; C. elegans; Delta 6 desaturase; CeD6.1; gamma-linolenic acid; GLA; plant fatty acid; octadecatetraenoic acid; OTA; elcosanoid; eczema; mastalgia; atherosclerosis; coronary disease; hypercholesterolaemia; diabetic neuropathy; viral infection; acne;
Claim 1; Fig 1; 44pp; English
                                                                                                                                                                                                                                                                                                                 Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans Delta 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polyunsaturated fatty acids, which can be used for treating malnutrition, in pharmaceutical compositions, in cosmetics or in animal feed. The polyunsaturated fatty acids can be used for treating e.g. restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enzyme. The specification describes methods for desaturating a fatty acid and for producing a desaturated fatty acid by expressing increased levels of a desaturase. Desaturases can be used for desaturating fatty acids. The enzymes can be used to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a peptide derived from a desaturase enzyme. The specification describes methods for desaturating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated fatty acid desaturase enzymes - use of polyunsaturated fatty acids for use in, e.g.
                              Desaturase enzymes, the genes encoding them and
                                                                 N-PSDB; AAX76589
                                                                                                                 Napier JA;
                                                                                                                                                                                  24-NOV-1997;
                                                                                                                                                                                                                 24-NOV-1998;
                                                                                                                                                                                                                                                   03-JUN-1999
                                                                                                                                                                                                                                                                                    W09927111-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY17751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY17751 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                 (UYBR-) UNIV BRISTOL
                                                                                                                                                                                                                                                                                                                                                    hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammatory skin disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGLNYQIEHHLFP
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                                                                                  1999-370905/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gglnyqiehhlfp
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nilarity 100.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pages 101-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                     cirrhosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nutritional compositions, cosmetics
                                                                                                                                                                                                                                                                                                                     elegans
                                                                                                                                                                                  97GB-0024783.
                                                                                                                                                                                                                 98WO-GB03507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300
                                                                                                                                                                                                                                                                                                                                                     cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 76; DB 19;
Pred. No. 1.7e-05;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    desaturase CeD6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used for the production
                                  their uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or animal feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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RESULT
AAY21891
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Best Local Similarity
Matches 13; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C. elegans delta 5-fatty acid desaturase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Delta 5-fatty acid desaturase; dihomogamma linolenic acid; arachidonic acid; cholesterol; polyunsaturated fatty acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           molecules may be used as anti-sense molecules to alter the expression (II) by binding to it and preventing transcription. Hybridizing molecules may also be provided as ribozymes which regulate expression
                                                                                                                                                                                 Michaelson L,
                                                                                                                                                                                                                                                                                                                             29-JUN-1998;
23-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9933958-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dietary supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY21891 standard; Protein; 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is Caenorhabditis elegans Delta 6 desaturase, designated CeD6.1. Desaturase enzymes (I) may be used as immunogens to
New isolated delta5-fatty acid desaturase enzymes useful in
                                                                           N-PSDB; AAX86961
                                                                                                             WPI; 1999-444067/37
                                                                                                                                                                                                                                                     (UYBR-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGLNYQIEHHLFP 13
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|78 gglnyqiehhlfp 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                         BRISTOL
                                                                                                                                                                                 Napier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       elegans
                                                                                                                                                                                                                                                                                                                         98GB-0014034.
97GB-0027256.
                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-GB03895
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                                                                                                                                                                                 JA,
                                                                                                                                                                                 Stobart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                 ζ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy;
foodstuff;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Best Local
         particular, the enzyme is useful for producing polyunsaturated fatty acids and for generating enzyme-specific antibodies useful for identifying desaturases. Oil-seed plants may be engineered to incorporate the enzyme, so that the plants produce seed oil rich in fatty acids. The fatty acids could be incorporated usefully into infant formula, foods of all kinds, dietary supplements, nutriceutical and pharmaceutical
                                                                                                     This is the Caenorhabditis elegans fatty acid delta-5 desaturase. The CDNA sequence is useful for recombinant production of the enzyme and i generating transformed host cells and transgenic plants. The desaturas can be used for creating a double-bond between two carbons. In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                where administration of polyunsaturated fatty acids may have beneficial disease-preventative effects. The polyunsaturated fatty acids can be used in foodstuffs or dietary supplements. The Delta 5-fatty acid desaturases can also be used for the synthesis of prostaglandins or modulation of the synthesis. The products can also be used for detection and diagnosis. The present sequence represents the C. elegans delta 5-fatty acid desaturase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mortierella alpina and Caenorhabditis elegans. The Delta 5 fatty acid desaturases catalyze the production of polyunsaturated fatty acids, e the conversion of dihomogamma linolenic acid to arachidonic acid. The
                                                                                                                                                                                                                  Purified protein having double-bond between two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C. elegans fatty acid delta-5-desaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes can be used in gene therapy as a preventative treatment, e.g. in patients suffering from high levels of cholesterol or other conditions
                                                                                                                                                                                     Claim 3; Fig
                                                                                                                                                                                                                                                                      N-PSDB; AAA51232
                                                                                                                                                                                                                                                                                   WPI; 2000-431293/37
                                                                                                                                                                                                                                                                                                                   Browse JA,
                                                                                                                                                                                                                                                                                                                                                                                                                  06-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fatty acid delta
infant formula;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY96721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY96721 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 18; Page 23; 36pp; English
                                                                                                                                                                                                                                                                                                                                                                                  07-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                  (UNIW ) UNIV WASHINGTON STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           delta-5 desaturase;
                                                                                                                                                                                                                                                                                                                   Wallis JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     447 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                     6A; 74pp;
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                                                                                                                                                                                                                                                                                                                                                                                  98US-0111301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dietary supplement
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                                                                                                                                                                                     English.
                                                                                                                                                                                                                      desaturase activity, carbons
                                                                                                                                                                                                                                                                                                                   Watts JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .0%; Score 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           447 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polyunsaturated;
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                                                                                                                                                                                                                                     useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oil;
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                                                                                                                                                                                                                                     creating
                                                                                                                         enzyme and for
the desaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                        This invention describes a novel sphingolipid desaturase that selectively introduces a double bond into the sphingobase of the ceramide residue of chirtoduces and capnoids. A DNA sequence encoding the sphingolipid CC desaturase, or a vector containing the DNA sequence, can be used to CC produce transgenic plants, especially crop plants, with an increased or CC decreased delta-8-unsaturated long-chain base content or an altered CC delta-8-unsaturated long-chain base content or an altered CC compensate for a delta-8-unsaturated long-chain base deficiency, to CC exclude production of delta-8-unsaturated bases, to increase tolerance CC or resistance to soil salinity, ion stress or toxicity, drought, wet CC conditions, cold or frost and/or phytopathogenic microorganisms, or to CC alter size growth and flowering time. Cells, transgenic organisms or CC plants containing the DNA sequence can be used to produce sphingolipids CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw CC materials. This sequence represents a protein which has delta6 fatty acid desaturase activity which is described in the method of the invention.
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid; transgenic plant; crop plant; delta-8-unsaturated long-chain base; tolerance; resistance; soil salinity; ion stress; toxicity; drought; cold; frost; phytopathogenic microorganism; flowering time; cosmetic
                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 16; 62pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New sphingolipid desaturase that selectively introduces double bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-127549/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heinz E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DE19828850-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY51355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        into sphingolipids and capnoids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUN-1998;
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                                                                                                                              454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      food; chemical raw material.
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
Score 76; Pred. No.
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Pred. No. 2.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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DB 21;
2.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                         Length 454;
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                                                                                                                                                                                               desaturase enzyme. The enzyme sequence is used in the methods of c the invention. The specification describes methods for desaturating a content of the invention. The specification describes methods for desaturating content of the invention of the producing a desaturated fatty acid by expressing content of the introduces of a desaturate. The present desaturate is an enzyme which introduces a double bond carbons 6 and 7 from the carboxyl end of cards. The enzyme can be used for desaturating fatty acids. The enzyme can be used for desaturating fatty conditions. The enzyme can be used for treating malnutrition, in pharmaceutical compositions, in cosmetics or in animal feed. The polyunsaturated fatty acids can be used for treating e.g. restenosis after angioplasty, can be used for treating the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the cond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fatty acid; delta-6 desaturase; polyunsaturated fatty acid; malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis; cancer; diabetes; eczema; platelet aggregation; vasodilation; cholesterol level; endometriosis; premenstrual syndrome; myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis; acute respiratory syndrome; hypertension; inflammatory skin disorder.
                                                                                            reduce or prevent gastro-intestinal bleeding and other side effects caused by non-steroidal anti-inflammatory drugs, prevent or treat endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis and chronic fatigue after viral infections, treat AIDS, multiple
                                                  disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Fig 3A-E; 165pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated fatty acid desaturase enzymes - used for the production of polyunsaturated fatty acids for use in, e.g. pharmaceutical compositions, nutritional compositions, cosmetics or animal feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chaudhary S, Thurmond J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A delta-6 desaturase enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a Mortierella alpina fatty acid delta-6
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(CALJ ) CALGENE LLC
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                                                                          acute respiratory syndrome,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0834655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                       hypertension
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                                                                          IDS, multiple and inflammatory skin
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               This represents a Mortierella alpina delta 6 desaturase. The invention crelates to a nucleic acid construct that contains at least one of the nucleotide sequences (AAX00889 to AAX00891) encoding M. alpina delta 6, cd delta 12 and delta 5 desaturases (AAW95504 to AAW95506) respectively. CC coupled to an expression control sequence functional in plants. CC Recombinant plant cells containing at least one DNA encoding a M. alpina fatty acid desaturase (FAD), can be used for the production of plants. CC polyunsaturated fatty acid (PUFA). These recombinant cells or plants cc containing them are used to produce oils such as linoleic acid, arachidonic acid, yamma-linolenic acid, dihomo-gamma-linolenic acid, containing them are used to produce oils such as linoleic acid, containing them are used to produce oils such as linoleic acid, containing them are used to produce oils such as linoleic acid, containing them are used to produce oils such as linoleic acid, containing them are used to produce oils such as linoleic acid, containing them are used to produce oils such as linoleic acid, containing all accompanies of the containing accompanies of the containing disorders associated with inadequate consumption or containing disorders associated with inadequate consumption or containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing and containing an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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11-APR-1997;
11-APR-1997;
11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic; stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula; dietary supplement; prostaglandin; restenosis; angioplasty; inflammation; rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chaudhary S, Thurmond J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ABBO
(CALJ
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Eig
                                                                                                                                                                                                                                                                                                                                                                                                                                             therapeutically, e.g. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plants - useful in human or animal nutrition,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid construct able to express fatty acid desaturase in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAX00889.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mortierella alpina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mortierella alpina delta 6 desaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW95504 standard; peptide; 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                390 gglnyqiehhlfp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGLNYQIEHHLFP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1999-080739/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 desaturase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABBOTT L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cosmetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    3A-E; 210pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Huang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAB.
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97US-0833610.
97US-0834033.
97US-0834655.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  animal feed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      recombinant; fatty acid desaturase; FAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100
    Fragments of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Knutzon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .08;
                                                                                                                                                                                                                                                                                                                                                                                                                                             restenosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 76;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leonard
    DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΑE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as
                                                                                                                                                                                                                                                                                                                                                                                                                                             cosmetics and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mukerji P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUFA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
The specification describes methods for desaturating a fatty acid and for producing a desaturated fatty acid by expressing increased levels of a desaturate. The present desaturates is an enzyme which introduces a double bond carbons 6 and 7 from the carboxyl end of a fatty acid molecule. The enzyme can be used for produce polyunsaturated fatty acids. The enzyme can be used for produce polyunsaturated fatty acids, which can be used for treating malnutrition, in pharmaceutical compositions, in commetics or in animal feed. The polyunsaturated fatty acids can be used for treating e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis, asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure. They can also be used to inhibit platelet aggregation, cause vasodilation, lower cholesterol levels, inhibit proliferation of vessel.
                                                                                                                                                                                                                                                                                                                                                            Chaudhary S, Thurmond J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer; diabetes; eczema; platelet aggregation; vasodilation;
cholesterol level; endometriosis; premenstrual syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A delta-6 desaturase enzyme amino acid sequence
                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                  used,
                                                                                                                                                                                                                                                                              New nucleic acid encoding delta5 and other desaturase enzymes useful in production of oils of increased arachidonic acid con
                                                                                                                                                                                                                                                                                                                               WPI; 1999-009334/01
                                                                                                                                                                                                                                                                                                                                                                                                        (ABBO ) ABBOTT LAB.
(CALJ ) CALGENE LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9846765-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acute respiratory syndrome; hypertension; inflammatory skin disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myalgic encephalomyelitis; chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                malnutrition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fatty acid; delta-6 desaturase; polyunsaturated fatty acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW85121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW85121 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plants can be engineered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             related coding sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     390 gglnyqiehhlfp 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            elated coding sequences. Recombinant plants can produce high yields of UFA, since new pathways can be created and unwanted ones suppressed. lants can be engineered to express oils of particular PUFA composition, g. one similar to that in human milk, and product recovery is simpler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGLNYQIEHHLFP 13
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                                                                                                                                                                                                                                                                e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e.g. fish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   457
                                                                                                                                                                                                                                                                for treating cancer,
                                                                                                                                                                                                                                   Pages 95-96; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                           Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US07422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                            Knutzon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rheumatoid arthritis; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 76;
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                                                                                                                                                                                                                                                                  foods,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fatigue; AIDS; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                           Leonard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 2.2e-05;
thes 0;
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                                                                                                                                                                                                                                                                    animal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              psoriasis;
                                                                                                                                                                                                                                                                    cosmetics
                                                                                                                                                                                                                                                                                 content,
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RESULT 1
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Best Local S
Matches 13
         The fatty acid desaturases are able to catalyse the conversion of oleic acid to linoleic acid, linoleic acid to gamma-linolenic acid or of alpha-linolenic acid to stearidonic acid. Transgenic insect cells
                                                                               Novel transgenic insect cells comprising a nucleotide sequences which encode delta-6-desaturase or delta-12- desaturase, useful for produci poly-unsaturated long chain fatty acids, e.g. arachidonic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     delta-6 desaturase; gamma-linolenic acid; biosynthesis; transgenic insect cell; polyunsaturated long chain fatty acid; antilnflammatory antirhemmatic; antiasthmatic; antipsoriatic; osteopathic; cytostatic; antidiabetic; dermatological; gynecological; anti-HIV; neuroprotective; hypotensive; nephrotropic; vasodilator;
                                                            Claim 1;
                                                                                                                                                  WPI; 2000-328935/28
                                                                                                                                                                          Mukerji P,
                                                                                                                                                                                                                            05-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiaggregant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY92599 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reduce or prevent gastro-intestinal bleeding and other side effects caused by non-steroidal anti-inflammatory drugs, prevent or treat endometriosis and premenstrual syndrome, treat myslgic encephalomyelitis and chronic fatigue after viral infections, treat AIDS, multiple
                                                                                                                                                                                                   (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                     29-SEP-1999;
                                                                                                                                                                                                                                                                                                       WO200020602-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mortierella alpina.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sclerosis, acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpina delta-6 fatty acid desaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
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                                                           Page 145-146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          457
                                                                                                                                                                         Huang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                            98US-0103110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vasotropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                  172..176
                                                                                                                                                                                                                                                                                                                                                      /label= histidine_box
/note= "conserved amo
395 ...399
                                                                                                                                                                                                                                                                                                                                                                                          /note= "conserved 209..213
                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             'note= "conserved among membrane-bound desaturases
                                                                                                                                                                                                                                                                                                                                           /label=
                                                                                                                                                                                                                                                                                                                                                                                                                   /label= histidine_box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             respiratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein; 457
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                                                                                                                                                                          Parker-barnes
                                                         170pp;
                                                                                                                                                                                                                                                                                                                                             histidine_box
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ral infections, treat AIDS, multiple syndrome, hypertension and inflammatory skin
                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 76;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
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                                                                                                                                                                          JM,
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thes 0;
                                                                                                                                                                                                                                                                                                                                                                                                        membrane-bound desaturases"
                                                                                                                                                                                                                                                                                                                                                                   membrane-bound
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                   desaturases"
                                                                                             for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC comprising a nucleotide sequence which encodes a polypeptide comprising CC residues 50-53, 39-43, 172-176, 204-213, or 390-402 of delta-6 cd desaturase (AAY92599) or comprising delta-12 desaturase (AAY92600) are C claimed. Oil and fatty acids (especially gamma-linolenic acid) isolated CC from the recombinant insect cells are also claimed. Production of CC polyunsaturated long chain fatty acids (PUFAS) in insect cells has many CC advantages, as insect cells have greatly simplified lipid compositions, are not subject to external variable fluctuations, and can easily be CC maintained and manipulated. The oils are used in pharmaceutical CC compositions, infant formulas, dietary supplements or substitutes, and CC cosmetics (all claimed). The PUFA supplements have antinflammatory, CC antirhemmatic, antiasthmatic, antipsoriatic, osteopathic, cytostatic, antidiabetic, dermatological, gynecological, anti-HIV, neuroprotective, Dypotensive, nephrotropic, vasodilator, antiaggregant and vasotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 13
            The invention relates to a method of generating novel compositions comprising animal cells producing essential fatty acids (FAs). The animal cells are produced by transforming cells, e.g. embryonic stem cells, with nucleic acid encoding heterologous enzymes involved in fatty acid, e.g. long chain or polyunsaturated fatty acid (PFA) biosynthesis. This sequence corresponds to a fungal delta6-desaturase whose coding sequence is an example of a nucleic acid sequence used to transform the cells. The essential FAs obtained can be used in nutritional formulations or animal feed formulations. The long chain PFAs can be used in nutritional
                                                                                                                                                                                                               Producing essential fatty acids and long-chain polyunsaturated fatty acids, for use in nutritional, animal feed and medical formulations
                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                   N-PSDB; AAZ47129
                                                                                                                                                                                                                                                                                                                                                                                       29-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                        28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fungal delta6-desaturase protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY56045;
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transgenic anima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 100 Local Similarity 100 Les 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
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                                                                                                                                                                                                                                                                                    2000-072619/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rated fatty acid; funguanimal; malnutrition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 457
                                                                                                                                                                                 Fig 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                 71pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein; 457
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                                                                                                                                                                                                                                                                                                                    Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fungus; delta6-des
tion; biosynthesis.
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Pred. No. 2.2
0; Mismatches
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                                                                                                                                                                                                                                                                                                                     Kirchner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         products can also be used for producing transgenic animals which can be used for producing essential FAs which can be used for producing downstream products such as leukotrienes, thromboxanes, arachidonic acid, elcosapentaenoic acid or docosahexaenoic acid. The products can also be used in cell culture. The animal or milk fat produced can be administered
                           polynucleotide sequence was used to trasfect mammalian cells, to produce animal cells expressing a desaturase gene and/or an elongase gene. Compositions comprising cells of the invention are useful for synthesising essential fatty acids, their derivatives or downstream products, as well as altered levels of long-chain polyunsaturated fatty acids and elcosanoids. The compositions are useful in nutritional formulae, e.g. infant formula, dietary supplements or dietary substitutes for both humans and animals. The compositions are also useful in cosmetic or animal feed formulations. Furthermore, the compositions may also be used as fat free media or as research reagents
                                                                                                                                                                                                                                                              New compositions comprising cells that express desaturases and elongases, for synthesizing essential fatty acids or long-chain polyunsaturated fatty acids, used in nutritional, cosmetic or animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eicosanoid; nutrition; infant for dietary substitute; animal feed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                delta6 desaturase; desaturase gene; elongase gene; fatty a elcosanoid; nutrition; infant formula; dietary supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB31684 standard; Protein; 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                 elongases, for synthesizing polyunsaturated fatty acids, feed formulations
                                                                                                                                                                                                                                                                                                                                 WPI; 2001-182622/18.
N-PSDB; AAF25234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JUL-2000; 2000WO-US19011.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to treat malnutrition
Sequence
                                                                                                                                                                                       The present sequence represents a delta6 desaturase. The desaturase
                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200104636-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of a fungal delta6 desaturase
                                                                                                                                                                                                                                                                                                                                                                              Kopchick JJ,
                                                                                                                                                                                                                                                                                                                                                                                                             OIHO AIND (-HOAD)
                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JUL-1999;
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nes 13; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12
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 457
                                                                                                                                                                                                                      Fig 9; 93pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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ches 0;
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Query Match

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gglnygiehhlfp GGLNYQIEHHLFP 13

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100.0%;

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                                                                              compensate for a delta-8-unsaturated long-chain base deficiency, to exclude production of delta-8-unsaturated bases, to increase tolerance or resistance to soil salinity, ion stress or toxicity, drought, wet conditions, cold or frost and/or phytopathogenic microorganisms, or to alter size growth and flowering time. Cells, transgenic organisms or plants containing the DNA sequence can be used to produce sphingolipids and capnolds with unsaturated sphingobases. The sphingolipids or capnoid
                                                                                                                                                                                                    desaturase, or a vector containing the DNA sequence, can be used to produce transgenic plants, especially crop plants, with an increased decreased delta-8-unsaturated long-chain base content or an altered delta-8-unsaturated long-chain base cris/trans ratio, especially to
                                                                                                                                                                                                                                                                   This invention describes a novel sphingolipid desaturase that select introduces a double bond into the sphingobase of the ceramide residusphingolipids and capnoids. A DNA sequence encoding the sphingolipid
                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 38-39; 62pp; German
                                                                                                                                                                                                                                                                                                                                                                     New sphingolipid desaturase that selectively introduces double bond into sphingolipids and capnoids -  \\
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transgenic plant; crop plant; delta-8-unsaturated tolerance; resistance; soil salinity; ion stress; cold; frost; phytopathogenic microorganism; flower pharmaceutical; food; chemical raw material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sphingolipid desaturase; sldl; sphingobase; ceramide; capnoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-APR-2000
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390 gglnyqiehhlfp 402
                               be used in cosmetics, pharmaceuticals and foods and as chemical raw erials. This sequence represents a protein which has delta6 fatty aciaturase activity which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGLNYQIEHHLFP
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473
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AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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; Mismatches 0;
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                                                                                 capnoids
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RESULT 15
AAY71551
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AAY96722
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                                                                                                    Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                   This is the Euglena gracilis fatty acid delta-8 desaturase. The cDNA sequence is useful for recombinant production of the enzyme and for generating transformed host cells and transgenic plants. The desaturase can be used for creating a double-bond between two carbons. In particular, the enzyme is useful for producing polyunsaturated fatty acids and for generating enzyme-specific antibodies useful for identifying desaturases. Oil-seed plants may be engineered to incorporate the enzyme, so that the plants produce seed oil rich in fatty acids. The fatty acids could be incorporated usefully into infant formula, foods of all kinds, dietary supplements, nutriceutical and pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= His-box_motif Misc-difference 358..362
                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 7A; 74pp;
                                                                                                                                                                                                                                                                                                                                                                           Purified protein having desaturase activity, useful for creating double-bond between two carbons
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-431293/37.
N-PSDB; AAA51233.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "encoded by GTG" Misc-difference 146..150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fatty acid delta-8 desaturase; polyunsaturated; oil; seed; infant formula; dietary supplement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E. gracilis fatty acid delta-8
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                                                                                                                                                                                             formulations.
                                                 353 gglnyqiehhlwp
                                                               1 GGLNYQIEHHLFP 13
                                                                                                                                                                    422 AA;
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                                                                                                     Conservative
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183..187
                                                  365
                                                                                                                93.48;
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                                                                                                    Score 71; DB 21;
Pred. No. 0.00015;
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                                                                                                                                                                                                                                            The present sequence is a delta-6 fatty acid desaturase protein sequence from clone pps.pk0011.d5:fis isolated from Florida bitterbush developing seed cDNA library, pps. The delta-6 desaturase enzyme catalyses the formation of tariric acid, a fatty acid that has a triple bond at the delta-6 carbon. The present sequence is useful for producing transgenic plants having altered levels of delta-6 desaturase which in turn would alter the fatty acid composition. The enzyme is also useful for producing polyclonal or monoclonal antibodies. The polynucleotide is useful as primer or probe for screening cDNA libraries to isolate desired full-length cDNA clones.
                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 10; Page 40-41; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polynucleotide encoding delta-6 desaturase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries -
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N-PSDB; AAD01349.
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acid; membrane-bound desaturase.
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Best Local Similarity
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Pred. No. 0.00082;
2; Mismatches 0;
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Result
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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US-08-333-11
US-09-363-574-10
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US-08-834-033A-6
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5.839 Million cell updates/sec
                                             Sequence 10, Appl Sequence 11, Appl Sequence 10, Appli Sequence 5, Appli Sequence 6, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 14, Appli Sequence 15, Appli Sequence 15, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 2, Appli Seque
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	38	38	38	38	41	47	47	47	58	58	58	58	58	58	58	60	60	64
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	23	22	22	22	268	252	252	252	446	446	186	186	125	125	125	448	448	365
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ALIGNMENTS	US-08-176-500-27	PCT-US95-11934-16	US-09-273-685-16	US-08-488-161-16	US-08-611-880-2	US-09-363-574-7	US-08-834-033A-8	US-08-834-655-7	US-08-834-033A-5	US-08-833-610-2	US-08-834-033A-13	US-08-833-610-3	US-09-363-574-8	US-08-834-033A-9	US-08-834-655-8	US-08-789-936-5	US-08-366-779-5	US-08-834-033A-17
	Sequence 27, Appl	Sequence 16, Appl	Sequence 16, Appl	16,	Sequence 2, Appli		Sequence 8, Appli	7,	Sequence 5, Appli	Sequence 2, Appli	Sequence 13, Appl	Sequence 3, Appli	Sequence 8, Appli	Sequence 9, Appli	Sequence 8, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 17, Appl

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TOPOLOGY: lin;

MOLECULE TYPE:
US-08-834-655-10
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US-08-834-655-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                  TELEX: N/A
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/8

FILING DATE: 11-APR-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: RAE-VENTER, BARBARA

NAME: RAE-VENTER, BARBARA
                                                                                                                                                                                                      REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (550) 328-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 260 SHE
CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                         TELEFAX:
                                                               STRANDEDNESS:
                                                                                     TYPE:
                                                                              amino acid
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                                                                                                                                                                                  (650) 328-4400
(650) 328-4477
                                           linear
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                   peptide
                                                               not relevant
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Query Match
Best Local Similarity
Matches 13; Conserv

100.0%; nilarity 100.0%; Conservative 0;

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Score 76; Pred. No. Mismatches 9 DB 2; .3e-07;

Length 87, Indels

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OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

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Patent No.
                                                                                                            Patent No.
                                                                                                                            Sequence 10,
                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/834,033A FILING DATE: 11-APR-1997 CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION: NAME: WARD, MICHAEL R. REGISTRATION NUMBER: 38,651 REFERENCE/DOCKET NUMBER: CGAB-300.US/TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 433-4150
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: N/A
INFORMATION FOR SEQ ID NO:
                                                            APPLICANT: APPLICANT:
                             APPLICANT:
 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
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22 GGLNYQIEHHLFP 34
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TOPOLOGY: lir
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                                                                                             INFORMATION:
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                                                                                                            0, Application US/09363574 6136574
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                          KNUTZON, DEBORAH
MURKERJI, PRADIP
HUANG, YUNG-SHENG
THURMOND, JENNIFER
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MUKERJI, PRADIP
HUANG, YUNG-SHENG
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                  CHAUDHARY,
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METHODS AND COMPOSITIONS FOR SYNTHESIS
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INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5968809
                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
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NAME: WARD, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                               COUNTRY: UZIP: 94306
                                                                                                                                                              STATE:
APPLICATION NUMBER: US/0 FILING DATE: 11-APR-1997
                                                                                                                                                                             CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 GGLNYQIEHHLFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/363,574
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                                                                                                                                                               CA
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                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                               MURKERJI, PRADIP
                                                                                                                                                                                                                                                                                               THURMOND, JENNIFER CHAUDHARY, SUNITA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
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100.0%;
                                                                                                                                                                                                                                                            METHODS AND COMPOSITIONS FOR SYNTHESIS OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
               US/08/834,655
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Pred. No. 9.3e-07;
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CLASSIFICATION:

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Query Match
Best Local Similarity
Watches 13; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08834033A Patent No. 6075183
                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
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TOPOLOGY: linear
MOLECULE TYPE: peptide
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TOPOLOGY: 1
MOLECULE TYPE:
                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
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                               TYPE: amino acid
STRANDEDNESS: not
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                                                                    LENGTH:
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                                                                  355 amino acids
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MUKERJI, PRADIP
                                                                                                                                      (415) 433-8716
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                               not relevant
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ER: CGNE.124.00US
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thes 0;
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-363-574-5
RESULT 7
US-08-834-655-2
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Best Local Similarity
Matches 13; Conserv
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
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                                                           288 GGLNYQIEHHLFP 300
                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 2001 FERKY E
                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/363,574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                        1 GGLNYQIEHHLFP 13
                                                                                                                                                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                            355 amino acids
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                                                                                                                                                                                                                                                                                                                                          (415) 433-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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HUANG, YUNG-SHENG
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                                                                                                                          Conservative
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                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 76; DB 3; 100.0%; Pred. No. 4.6e-06;
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                                                                                                                     Score 76; DB 4; Pred. No. 4.6e-06;
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                                                                                                                                                   Length 355;
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                                                                                                                      Gaps
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Sequence 2, Application US/08834655
Patent No. 5968809
GENERAL INFORMATION:

APPLICANT:

KNUTZON, DEBORAH

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 13;
                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                              TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEPAX: (650) 328-4477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
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MEDIUM TYPE: Floppy
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TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
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                                                                                          STREET: 260 SHEI
CITY: PALO ALTO
STATE: CALIFORN:
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                                                                      COUNTRY: USA
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ZIP: 94306
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                                                                                                                                             ADDRESSEE:
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                                                          94306
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                                                                                          CALIFORNIA
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                                                                                                                         E: RAE-VENTER LAW GROUP, P.C.
260 SHERIDAN AVE, P.O. BOX 60039
                                                                                                                                                                                                                                 MURKERJI, PRADIP
HUANG, YUNG-SHENG
THURMOND, JENNIFER
CHAUDHARY, SUNITA
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Pred. No. 6.2
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
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Best Local :
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              TELEFAX: (415) 433-871
TELEX: N/A
INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US_08/834,0:
FILING DATE: 11-APR-1997
                                                                                                                                                                                                                                                                                         ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)328-4400
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CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS
                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
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LENGTH: 457 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS NUMBER OF SEQUENCES: 26
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                                                                                                                                                              CLASSIFICATION: 800
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STRANDEDNESS: not
TOPOLOGY: linear
                                                                                                                 REGISTRATION NUMBER: 38,651
                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: LIMBACH AND LIMBACH, L.L.P STREET: 2001 FERRY BUILDING
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MUKERJI, PRADIP
HUANG, YUNG-SHENG
                                                                                                                                                                                                                                                                                                                                                 USA
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                                                (415) 433-8716
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PatentIn Release #1.0, Version #1.30
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                                                                                                      CGAB-300.USA
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Pred. No. 6.2e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 457;
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; MOLECULE TYPE: peptide
US-08-834-033A-2
RESULT
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                                                                                                                 Best
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                                                                                                                               Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/834
EILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 457 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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                                         390 GGLNYQIEHHLFP 402
                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                            TELEFAX: ('TELEX: N/A
                                                                                                                Local
                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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STRANDEDNESS: no
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                                                                     1 GGLNYQIEHHLFP 13
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                                                                                                                Similarity
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HUANG, YUNG-SHENG
                                                                                                                                                                                                                                                                                                         (415) 433-8716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                    Conservative
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                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/834,033A
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                                                                                             Score 76; DB 3, Pred. No. 6.2e-06;
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Pred. No. 6.2e-06;
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                                                                                                                           Length 457;
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RESULT 12
US-08-833-610-5
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                       NUMBER OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T
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APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
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LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
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CITY: SAN FRANCISCO
STATE: CA
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CALIFORNIA
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MURKERJI, PRADIP
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY:

94306

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Best Local Similarity
Matches 11; Conserv
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                                                                                                SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KNUTZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
            ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300.USA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
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                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE:
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                                                                                                                                                                                                                                                                                                  STATE:
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                                                                                                                                                                                                                                                                                USA
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84.6%;
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Pred. No.
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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-834-655-9
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US-08-834-655-9
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US-08-834-033A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Applic
Patent No. 5968809
   Matches
                              Query Match
Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY AND THE CHAIN POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-UNSATURATED FATTY POLY-U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368 GGLQFQIEHHLFP 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U:
ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: RAE-VENTER LAW GROUP, P.C. STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                           LENGTH:
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                                                                                                                                                                                                                                                                                                                       131 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       (650) 328-4477
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THURMOND, JENNIFER
CHAUDHARY, SUNITA
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MURKERJI, PRADIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNUTZON, DEBORAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                 84.2%;
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                                    Score 64; I
Pred. No. 0
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Pred. No.
   Mismatches
                                                                   DB 2;
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                                                            Length 131;
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Gaps
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   0;
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1 GGLNYQIEHHLFP 13

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CALL: SAN COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDDERFECT 5.1
CURRENT APPLICATION UNMBER: US/08/834,033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: GGAB-300.USA
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 433-4150
TELEX: N/A
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULAR TYPE: peptide
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Search completed: August 9, 2001, 20:25:07 Job time: 206 sec
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// MOLECULE TYPE: peptide
US-08-834-033A-10
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US-08-834-033A-10
                                                                                                                                                                              Query Match
Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MUKERI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
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89 GHLNFQIEHHLFP 101
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89 GHLNFQIEHHLFP 101
                                                                                                                                                                              Conservative
                                                                                                                                                                                                 84.2%;
                                                                                                                                                                                               Score 64; DB 3;
Pred. No. 0.00021;
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pir3:*
                          pir1:*
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19.536 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	2 2	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	1		Result
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T31123	E64815	D85587	T32554	T29409	T27158	T01936	JC5646	T40333	T11220	C86704	S77365	G82323	S75038	T11959	G70590	B83034	JC7556	S68358	T50555	T47950	A84900	JG0180	T13155	S54809	S35157	T36617	T26280	T43319	110	;
hypothetical prote	_	ī			hypothetical prote	probable ethylene-	interleukin-1 beta	probable fatty aci	reverse transcript	conserved hypothet	hypothetical prote	conserved hypothet	hypothetical prote	id desa	probable desA3 pro	conserved hypothet	linoleoyl-CoA desa	S	delta-8 sphingolip	\supset	tical	Delta6 fatty acid	linoleoyl-CoA desa	linoleoyl-CoA desa	atty aci	probable Delta6 fa	oyl-co <i>l</i>	Delta5 fatty acid	pescription	7

linoleoyl-CoA desaturase (EC 1.14.99.25) W08D2.4 - Caenorhabditis elegans N;Alternate names: Delta6 fatty acid desaturase C;Species: Caenorhabditis elegans C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000 C;Accession: T26280; T37238 R;Swinburne, J.; Ainscough, R.

R;Swinburne, J.; Ainscough, R. submitted to the EMBL Data Library, March 1996

Z20188

A; Reference

T26280

RESULT T26280

5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
38.5	38.5	39	39	39	39	39	39	39	39	39	39.5	39.5	39.5	40	40
50.7	50.7	51.3	51.3	51.3	51.3	51.3	51.3	51.3	51.3	51.3	52.0	52.0	52.0	52.6	52.6
367	333	4056	988	685	405	382	373	325	325	320	1142	1003	674	744	482
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S55961	T26230	н96599	S35362	C70678	QQBE35	D72513	S65583	G72020	F86605	F96745	T39103	S07526	S32230	B64049	S22654
hypothetical prote	hypothetical prote	protein F14J16.10	protein kinase C (probable electron	BBRF3 protein - hu	probable aminopept	mating type protei	3′(2′),5′-bisphosp	sulfite synthesis/	unknown protein T9	probable negative	Ca2+-transporting	Ca2+-transporting	outer membrane pro	ARS-binding factor

ALIGNMENTS

Ş A;Map position: 4
A;Map position: 4
A;Introns: 43/3; 80/3; 197/3; 295/3; 318/2; 349/1; 384/3
C;Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
C;Keywords: oxidoreductase; unsaturated fatty acid biosynthesis A;Title: Functional identification of a fatty acid delta5 desaturase gene from Caenor A;Reference number: 222422; MUID:99059458
A;Accession: T43319 C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000 C;Accession: T43319; T24875 R;Michaelson, L.V.; Napier, J.A.; Lewis, M.; Griffiths, G.; Lazarus, C.M.; Stobart, A FEBS Lett 439, 215-218, 1998 Вb A; Molecule type: DNA A; Residues: 1-197, 'VSHIFNN', 198-447 <WIL> submitted to the EMBL Data Library, October 1996 A; Reference number: Z19947 Delta5 fatty acid desaturase (EC 1.14.99.-) T13F2.1 [validated] - Caenorhabditis eleg C;Species: Caenorhabditis elegans A;Gene: CESP:Tl3F2.1; des-5 C; Genetics A; Reference number: A; Accession: T24875 R;Swinburne, A;Cross-references: EMBL:AF078796; NID:g4003522; PIDN:AAC95143.1; PID:g4003523 A; Molecule type: mRNA A; Residues: 1-447 <MIC> A; Experimental source: clone T13F2 A;Cross-references: EMBL:Z81122; A; Status: preliminary; translated from GB/EMBL/DDBJ A;Status: translated from GB/EMBL/DDBJ Best Local Similarity 100.0%; Score 76; DB 1; Best Local Similarity 100.0%; Pred. No. 8.5e-06; Matches 13; Conservative 0: Mismatches 1 GGLNYQIEHHLFP 13 PIDN:CAB03352.1; GSPDB:GN00022; CESP:T13F2.1 Length 447; Indels 0; Gaps 0

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C;Species: Synechocystis sp.
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C;Accession: S35157; S76243
R;Reddy, A.S.; Nuccio, M.L.; Gross, L.M.; Thomas, T.L.
Plant Mol. Biol. 22, 293-300, 1993
A;Title: Isolation of a Delta(6)-desaturase gene from the cyanobacterium Synechocystis A;Reference number: S35157; MUID:93283633
A;Accession: S35157
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                           RESULT
S35157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;cluss*references: EMBL:AL078610; PIDN:CAB44385.1; GSPDB:GN00070; SCOEDB:SCH35.42c
A;Experimental source: strain A3(2)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Introns: 13/3; 39/2; 234/3; 277/3; 378/1; 413/3
C;Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
C;Keywords: alternative splicing; oxidoreductase; unsaturated fatty acid biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable Delta6 fatty acid desaturase (EC 1.14.99.-) SCH35.42c [similarity] -
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
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A;Title: Identification of a caenorhabditis elegans Delta6-fatty-acid-desaturase
A;Reference number: 221637; MUID:98149727
A;Accession: T37238
                                                                                                                                                                                                               Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] -
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C; Keywords:
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A; Residues: 1-345 <OLI>
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R; Oliver, K.; Harri
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A;Gene: CESP:W08D2.4
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A;Residues: 1-38,69-430,'V',432-473 <NAP>
A;Cross-references: EMBL:AF031477; NID:g3
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A;Molecule type: DNA
A;Residues: 1-473 <WIL>
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Matches 13
Status: preliminar: Molecule type: DNA
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nes 12; Conserv
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R:Tasaka, Y.
submitted to the EMBL Data Library, Ma
A:Reference number: S54809
A:Accession: S54809
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-368 CTAS>
A:Residues: 1-368 CTAS>
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A;Accession: S76243
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-359 <KAN>
                                                                                                                                         R:Cho, H.P.; Nakamura, M.T.; Clarke, S.D.
J. Biol. Chem. 274, 471-477, 1999
A:Title: Cloning, expression, and nutritional regulation A; Reference number: 217612; MUID:99085046
A; Accession: T13155
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C;Species: Spirulina platensis
C;Date: 08-Jul-1995 #sequence_revisic
C;Accession: S54809
A;Cross-references: EMBL:AF126799; NID:g4406527; PID:g4406528; PIDN:AAD20018. R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, March 1999 A;Reference number: Z16471
                                                                               A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-444 <CHO>
                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999
C;Accession: T13155; T08765
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S54809
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 C;Keywords: oxidoreductase; unsaturated fatty acid biosynthesis
                                                                                                                                                                                                                                                                                                             linoleoyl-CoA desaturase (EC 1.14.99.25) [validated] - human
N;Alternate names: Delta6 fatty acid desaturase; protein DKF
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A; Cross-references: GB:
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Best Local Similarity
Matches 11; Conserv
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Best Local
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                                                                                                                                                                                         the mammalian Delta-6
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A;Gene: GDB:FADSD6
A;Cross-references: GDB:9956652
A;Note: DKFZp586C201.1
A;Note: DKFZp586C201.1
C;Superfamily: cytochrome b5 core homology
C;Keywords: Chromoprotein; heme; iron; metalloprotein; oxidoreductase; u
C;Keywords: cytochrome b5 core homology <CB5>
F;18-94/Domain: cytochrome b5 core homology <CB5>
F;53,76/Binding site: heme iron (His) (axial ligands) #status predicted
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A;Residues: 1-444 <AKI>
A;Residues: 1-444 <AKI>
A;Cross-references: DBJ:AB021980; NID:94514721; PIDN:BAA75496.1; PID:94514722
C;Superfamily: cytochrome b5 core homology
C;Keywords: heme; iron; metalloprotein; oxidoreductase; unsaturated fatty acid biosynthe
C;Keywords: heme; iron; metalloprotein; oxidoreductase; unsaturated fatty acid biosynthe
F:18-94/Domain: cytochrome b5 core homology <CB5>
F:53,76/Binding site: heme iron (His) (axial ligands) #status predicted
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A;Title: Molecular cloning and functional characterization of rak;Reference number: JGO180; MUID:99160394
A;Accession: JGO180
A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change C;Accession: JG0180
                                                                         A; Molecule type: D
A; Residues: 1-449
                                                                                                                                                                                                                                                                                                                                  R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Talleuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Verens, J.A.; Salzberg, S.L.; Fraser, J.A.; Salzberg, S.L.; J.A.; Salzberg, S.L.; Fraser, C.M.; Verens, J.A.; Salzberg, S.L.; Fraser, J.A.; Salzberg, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein At2g46210 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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C;Genetics:
                                                                                                                                                                                          A; Accession: A84900
                                                                                                                                                                                                                             A; Reference number: A84420;
                                                                                                                                                                                                                                                                A; Title: Sequence and analysis of chromosome
                                                                                                                                                                                                                                                                                                   Nature 402, 761-768, 1999
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                                                                                                                                                   Status: preliminary
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                                                                             <STO>
                                      GB:AE002093; NID:g3702328; PIDN:AAC62885.1; GSPDB:GN00139
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iron (His) (axial ligands) #status predicted
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Pred. No.
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Pred. No.
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0.0012;
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A;Experimental source: cultivar Columbia; BAC clone F2;
R;Sperling, P.; Zaehringer, U.; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A;Title: A sphingolipid desaturase from higher plants.
A;Reference number: Z22986; MUID:99003197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            delta-8 sphingolipid desaturase (EC 1.14.99.-) [validated] - N;Alternate names: protein F2A19.180 C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                               R;Sperling, P.; Zaehilnger, U.; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A;Title: A sphingolipid desaturase from h
A;Reference number: Z22986; MUID:99003197
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                A; Cross-references:
                                      A; Residues: 1-449 <SPE>
                                                    A;Status: preliminary; translated A;Molecule type: mRNA
                                                                                            A; Accession: T50555
                                                                                                             A; Reference number:
                                                                                                                                                                                           C; Accession:
                                                                                                                                                                                                            C; Date: 21-Jul-2000 #sequence_revision 21-Jul-2000
                                                                                                                                                                                                                              delta-8 sphingolipid desaturase [imported] - rape
C; Species: Brassica napus (rape)
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A;Experimental source: cultivar Columbia; mainly green
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A; Residues: 1-449 <SP
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A;Molecule type: DNA
A;Residues: 1-449 <DEH>
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A; Experimental source: cultivar
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F2A19.180
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                EMBL: AJ224160; PIDN: CAA11857.1
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76.9%;
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76.9%;
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evision 20-Apr-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 64; DB 2;
Pred. No. 0.0012;
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Pred. No. 0.0012;
                                                                        from GB/EMBL/DDBJ
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RESULT
B83034
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A;Title: Delta6-desaturase of Mucor rouxii with high similarity to plant delta6-desatura A;Reference number: JC7556; MUID: 20563795
A;Accession: JC7556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Cross-references: EMBL:x87143; NID:g1040728; PIDN:CAA60621.1; PID:g1040729 C;Superfamily: cytochrome b5 core homology C:Keywords: heme; iron; metalloprotein; oxidoreductase F:16-90/Domain: cytochrome b5 core homology <CB5> F:51,74/Binding site: heme iron (His) (axial ligands) #status predicted
                                                                                                       Š
                                                                                                                                                                                                                                 A;Cross-references: GB:AF290983
A;Experimental source: strain ATCC 24905
C;Comment: This enzyme, a membrane-bound key enzyme,
C;Keywords: transformation; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 31-Mar-2001
C;Accession: JC7556
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A;Molecule type: mRNA
A;Residues: 1-458 <SPE>
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C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
                                                                          В
                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-523 < LAO>
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J. Biochem. 232, 798-805, 1995
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76.9%;
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A;Status: preliminary;
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conserved hypothetical protein PA4888 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: B83034 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M. adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lory, S.; Olson, M.V. Riture 406, 959-964, 2000
                                               fatty-acid desaturase - red alga (Cyanidium caldarium) chloroplast C;Species: chloroplast Cyanidium caldarium C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-C;Accession: T11959
C;Accession: T11959
R;Gloeckner, G.; Rosenthal, A.; Valentin, K. submitted to the EMBL Data Library, September 1997
A;Description: Organisation of 46 kb of the Cyanidium caldarium RKI
A; Description: Organisation A; Reference number: 217374 A; Accession: T11959
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A;Experimental source: strain H37Rv
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A; Residues: 1-427 <COL>
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Hamris, D.; ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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A; Residues: 1-370 <STO>
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A;Reference number: A82950;
A;Recession: B83034
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69.2%;
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69.2%;
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Pred. No.
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Pred. No.
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translated from GB/EMBL/DDBJ

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A; Molecule type: DNA
A; Residues: 1-287 <GLO>
A; Cross-references: EMBL: AF022186; NID: g2465730; PIDN: AAB82698.1; PID: g2465769
A; Cross-references: Extrain RK1
C; Genetics:
A; Gene: desA
A; Genome: chloroplast
C; Keywords: chloroplast
C; Keywords: chloroplast
Ouery Match
Best Local Similarity 58.3%; Pred. No. 1.9;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Search completed: August 9, 2001, 20:26:08
Job time: 247 sec
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August 9, 2001, 20:36:51; Search time 28.86 Seconds (without alignments) 15.430 Million cell updates/sec
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Title:
Perfect score:
Sequence: US-09-367-013B-2_COPY_390_402 GGLNYQIEHHLFP 13

Scoring table: BLOSUM62

93435 seqs, 34255486 residues Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_39:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1 GGLNYQIEHHLFP 13

Query Match 84.2%; Score 64; DB 1; Length 359; Best Local Similarity 76.9%; Pred. No. 0.00091; Matches 10; Conservative 2; Mismatches 1; Indels

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ALIGNMENTS

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EMBL; L11421; AAA27286.1; EMBL; D90914; BAA18502.1; Oxidoreductase; Iron. SEQUENCE 359 AA; 41425 MW; 33FB165AEB98C05F CRC64;	right. It of Bioinfo nstitute. ions as lo s not remo greement (gb-sib.ch)	"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).	SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINB-97061201; PubMed-8905231; Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.,	UENCE FROM N.A. LINE-93283633; PubMed-8389613; dy A.S., Nuccio M.L., Gross L.M., Thomas T.L.; olation of a delta 6-desaturase gene from the cyanobacterium echocystis sp. strain PCC 6803 by gain-of-function expression baena sp. strain PCC 7120."; baena sp. strain PCC 7120.";	LLCD_SYNY3 LLCD_SYNY3 DLCD_SYNY3 STANDARD; PRT; 359 AA. AC Q08871; DT 01-NOV-1997 (Rel. 35, Created) DT 01-NOV-1997 (Rel. 35, Last sequence update) DT 01-NOV-1997 (Rel. 35, Last annotation update) DT LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE). GN DES6 OR SLL0262. GS Synechocystis sp. (strain PCC 6803). Synechocystis sp. (strain PCC 6803). CC Bacteria; Cyanobacteria; Chroococccales; Synechocystis. OX NCBL_TaxID=1148;

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GGLNHQVTHHLFP

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RESULT 2
IL1B_HORSE
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15-DEC-1998 (Rel
15-DEC-1998 (Rel
30-MAY-2000 (Rel
                                                                                      EMBL;
                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
             PRINTS; PR00262; IL1HBGF.
PRINTS; PR00264; INTERLEUKIN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (SHORT FORM).
MEDLINE-97080493; Pubmed-8921838;
METO-1., Youn H.Y., Ohashi T., Watari T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Howard R.D., McIlwraith C.W., Trotter G.W., Nyborg J.K.; "Cloning of equine interleukin-1 alpha and equine interleukin-1 and determination of their full-length cDNA sequences.";
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Metazoa; Chordata;
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15-DEC-1998 (Rel. 37, Last sequence updat
30-MAY-2000 (Rel. 39, Last annotation upd
INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
                                                         InterPro; IPR002348;
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3ene 177:11-16(1996)
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- SUBUNIT: MONOMER (BY S)
- ALTERNATIVE PRODUCTS: 1
SPLICING.
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                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY. IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
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                                                                                                   BAA07718.1; -.
AAC39256.1; -.
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OShima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itob T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Mashimoto H., Nishio Y., Saito N
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                          use by non-profit institutions as long as modified and this statement is not removed. U
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DR
SQ
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                          Oberye E.H.H., Maurer K., Mager W.H., Planta R.J.;
"Structure of the ABF1-homologue from Kluyveromyces marxianus.";
Biochim. Biophys. Acta 1173:233-236(1993).
-I- FUNCTION: TRANS-ACTING FACTOR IN THE REGULATION OF TRANSCRIPTION AND IN DNA REPLICATION. INVOLVED IN THE TRANSCRIPTION ACTIVATION.
OF A SUBSET OF RIBOSOMAL PROTEINS GENES. BYMDS THE ARS-ELEMENTS
FOUND IN MANY PROMOTERS. BINDS TO THE SEQUENCE 5'-TCN(7)ACG-3'.
-I- SUBCELLULAR LOCATION: NUCLEAR.
-I- PTM: EXYENSTYELY PHOSPHORYLATED ON SER AND THR RESIDUES
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN-CBS 2359 / IFO 1267 / NRRL Y-1140;

MEDLINE-92279012; PubMed-1594441;

Goncalves P.M., Maurer K., Mager W.H., Planta R.J.;

"Kluyveromyces contains a functional ABF1-homologue.
Nucleic Acids Res. 20:2211-2215(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1992 (Rel. 23, Created)
01-FEB-1994 (Rel. 28, Last sequence upc
15-DEC-1996 (Rel. 37, Last annotation upc
TRANSCRIPTION FACTOR BAF1 (ARS BINDING
(BIDIRECTIONALLY ACTING FACTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Transferase. SEQUENCE 413 AA; 47633 MW; 74998B2A1AD24A11 CRC64;
   MOD_RES
SEQUENCE
                                                                                                                                                                                         modified and this statement
                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab
between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharor
Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAF1_KLULA
P26375;
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InterPro; IPR001736; -.
Pfam; PF00614; PLDc; 2.
                                                                                                                                                             or send
                                                                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS TO C-TERMINUS.
MEDLINE=93277959; PubMed=7916634;
                                                          Frans-acting
                                                                           Phosphorylation;
                                                                                       franscription regulation; Activator;
                                                                                                      fransfac; T01240;
                                 DOMAIN
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                                                                                                                                                                                                                                                                          SIMILARITY: STRONG TO YEAST BAF1, AND LOCAL TO YEAST RAP1
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                                                                                                                   S22654;
                                                                                                                                 X64462; CAA45792.1;
                                                                                                                                                            s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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                                                                                                                   S22654.
                                                          factor.
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                                                                        Zinc-finger; Metal-binding;
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28, Last sequence update)
37, Last annotation update
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77.8%;
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ASP/GLU-RICH.
PHOSPHORYLATION (
E5CFF6056EA901F
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Pred. No. 9.2;
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                                                                      DNA-binding; Nuclear protein;
binding; Zinc; DNA replication
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CRC64;
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Query Match

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RESULT 5
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ID HXC1_HAEIN
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Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Potton M.D., Control of the C.D., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Potton M.S., Control of the C.D., Smith H.O., Small K.V., Fraser C.M., Smith H.O., Potton M.S., Control of the C.D., Smith H.O., Potton M.S., Control of the C.D., Smith H.O., Potton M.S., Control of the C.D., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Potton M.S., Control of the C.D., Control of the C.D., Potton M.S., Control of the C.D.,                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00430; TONB_DEPENDENT_REC_1; FALSE_NEG PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Outer membrane; Transport; TonB box; Signal; Rece
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00593; TonB_boxC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U32696; AAC21789.1; TIGR; HI0113; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=95350630; PubMed=75428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995
01-NOV-1997
                                                                                                                                                                                                                                                                 SEQUENCE
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SUBCELLULAR LOCATION: OUTER MEMBRANE (BY SIMILARITY).
SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
SIMILARITY: LOCAL TO OTHER CORRESPONDING PROTEIN IN SEROTYPE B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Elemopean Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: LOW, H.INFLUENZAE.
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                                 GLNYQIEHHL
GLNYDVNHYL
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Pred. No.
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HEME/HEMOPEXIN UTILIZATION PROTEIN
74D94F72E41AEC31 CRC64;
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A., Merrick J.M.,
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RESULT
ATC_ARS
Magnesium; ATP-binding; A
DOMAIN 1 59
TRANSMEM 60 78
DOMAIN 79 89
DOMAIN 90 110
DOMAIN 111 262
TRANSMEM 263 282
TRANSMEM 263 300
TRANSMEM 301 318
DOMAIN 319 775
TRANSMEM 375 799
DOMAIN 800 840
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P35316;
01-FEB-1994
                                                                                                                                                                                                                                                          EMBL; X51674; CAA35980.1; -. EMBL; X72713; CAA51262.1; -. PIR; S07526; S07526.
                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
CALCIUM-TRANSPORTING ATPASE SARCOPLASMIC/ENDOPLASMIC RETICULUM TYPE
(EC 3.6.1.38) (CALCIUM PUMP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Palmero I., Sastre L.;
"Complementary DNA cloning of a protein highly homologous to mammalian sarcoplasmic reticulum Ca-ATPase from the crustacean
                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                PRINTS; PROO119; CATATPASE.
PROSITE; PSO0154; ATPASE_E1_E2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93300797; PubMed=8314776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 354-1003 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Artemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;
Artemildae; Artemia.
                                                                                                                                                                                                                               Pfam; PF00122; E1-E2_ATPase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escalante R., Sastre L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-90133927; PubMed-2533270;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Artemia sanfranciscana (Brine shrimp) (Artemia franciscana
                                                                                                                                                                                                                                            nterPro; IPR001757; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Biol. 210:737-748(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATIVE PRODUCTS: TWO ISOFORMS ARE PRODUCED BY ALTERNATIVE SPLICING. THE 2 FORMS DIFFER ONLY IN THEIR C-TERMINAL AMINO ACIDS. THE LONGER FORM PRESENTS AN EXTENSION, A POTENTIAL TRANSMEMBRANE DOMAIN, WHICH MAY HAVE AN IMPORTANT FUNCTIONAL ROLE. DEVELOPMENTAL STACE: ISOFORM 2 (LONG FORM) IS EXPRESSED ONLY IN EARLY STAGES OF EMBRYONIC DEVELOPMENT (CYSTS), WHILE ISOFORM 1 (SHORT FORM) IS ALSO FOUND IN LATER EMBRYONIC STAGES AND ADULTS. SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RETICULUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                           (E1-E2 ATPASES).
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                                                                                                                                                                                 Calcium transport; Transmembrane; Phosphorylation;
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                                                                                                                                                                   Alternative splicing
 EXTRACELLULAR (POTENTIAL)
                               CYTOPLASMIC (POTENTIAL)
                                             POTENTIAL
                                                            EXTRACELLULAR (POTENTIAL)
                                                                            POTENTIAL.
                                                                                        CYTOPLASMIC (POTENTIAL)
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Best Local
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Q10115;
01-FEB-1996
01-FEB-1996
01-OCT-2000
MATING TYPE
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CONFLICT
SEQUENCE
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DOMAIN
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                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                              MEDLINE-96204518; PubMed-8628238; Ferreira A.V.B., Saupe S., Glass N.L.; Ferreira A.V.B., Saupe S., Glass N.L.; Intercept analysis of the mta idiomorph identifies two genes in addition to mta-1."; Mol. Gen. Genet. 250:767-774(1996).
-i- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-i- SIMILARITY: TO P.ANSERINA SMR1.
                                                                                                                                                                                                                                                                                                                                                                                           Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                  Sordariales; Sordariaceae;
NCBI_TaxID=5141;
                                                                                                         SEQUENCE
                                                                                                                     Nuclear protein
                                                                                                                                Fertilization; Transcription
                                                                                                                                           EMBL; M33876; AAC37477.1;
                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                STRAIN=74-OR23-1A;
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                                                         Local
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GGRNWHVDHTLHP
                      GGLNYQIEHHLFP
                                            6; Conserv
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                                              Conservative
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(Rel. 33, Last sequence update)
(Rel. 40, Last annotation update)
PROTEIN A-2 (MT A-2) (UPPER CASE "A").
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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72.7%;
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                                                          Score 39; Pred. No.
                                                                                                                                regulation; Activator; DNA-binding;
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Pred. No. 41;
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EFSFIK -> GMPLSSYFVDAWGLVLAWALFFGVIFYSPL
(IN SECOND ISOFORM).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                         CF1FED8041009FC0 CRC64;
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                                                Mismatches
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RESULT

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21-JUL-1986
01-APR-1993
                   01-JUN-1994 (Rel. 29, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
PROTEIN KINASE C-LIKE 1 (EC 2.7.1.-)
PCK1 OR SPAC22H10.01C OR SPAC17G8.14C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                      PCK1_SCHPO
P36582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM CARBOHYD
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MEDLINE-84270667; PubMed-6087149;
Baer R., Bankler A.T., Biggin M.D., De
Gibson T.J., Hatfull G., Hudson G.S.,
Tuffnell P.S., Barrell B.G.;
"DNA sequence and expression of the BS
Nature 310:207-211[1984].
                                                                                                                                                                                                                                 SCHP0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01528; Herpes_glycop; PRINTS; PR00333; HSVINTEGRLMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; dsDNA viruses,
Gammaherpesvirinae; Lymp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Epstein-barr virus (strain Viruses; dsDNA viruses, no
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  Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
-!- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEIN
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by non-profit institutions as long as its content
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Prone; Glycoprotein;
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6 (Rel. 01, Last sequence)
3 (Rel. 25, Last annotin M.
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ses, no RNA stage; Herpesviridae;
Lymphocryptovirus.
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60.0%;
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Pred. No. 20;
1; Mismatches
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N-LINKED (GLCNAC. . .) (PO
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25A8A46B6CDCOAE1 CRC64;
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(Rel. 35, Created)

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Matches 7
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InterPro; IPR000961; -.
InterPro; IPR002219; -.
InterPro; IPR002290; -.
Pfam; PF00130; DAG_PE-bind; 2
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NP_BIND
BINDING
ACT_SITE
CONFLICT
SEQUENCE
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Pfam; Pro0069; pkinase; 1.

Pfam; Pr00433; pkinase_C; 1.

Pfam; Pr00433; pkinase_C; 1.

PROSITE; PS00479; DAG_PE_BIND_DOM_2; 2.

PROSITE; PS00101; PROTEIN_KINASE_ATP; 1.

PROSITE; PS0011; PROTEIN_KINASE_ST; 1.
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MEDLINE-93259141; PubMed-8491190;

MEDLINE-93259141; PubMed-8491190;

Toda T., Shimanuki M., Yanagida M.;

Toda T., Shimanuki M., Yanagida M.;

"Two novel protein kinase C-related genes of fission yeast are

essential for cell viability and implicated in cell shape control.";

EMBO J. 12:1987-1995(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D14337; BAA03267.1;
EMBL; Z69730; CAA93602.1;
EMBL; Z69795; CAA93697.1;
EMBL; S35362; S35362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deviin K., Churcher C.M., Barrell B.G., Rajandream M.A., Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: INVOLVED IN THE CONTROL OF THE CELL SHAPE.
OF THE INHIBITOR STAUROSPORINE.
-i- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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473
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ATP (BY SIMILARITY).
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AMVASTKNP -> SNGGFDGE
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Pred. No.
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PHORBOL-ESTER
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PROTEIN KINASE
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49;
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k/DDBJ databases.
F THE CELL SHAPE.
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MEDLINE=99039499; PubMed=9823893; Andersson J.O., Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RS7_RICPR STANDARD;
P41081;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last seg
30-MAY-2000 (Rel. 39, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D., Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso Rifken L., Riles L., Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R., Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases P. SIMILARITY: BELONGS TO THE UPF0034 (NIFR3/SMM1) FAMILY.
                                                                                                                                                                                                                              Submitted (OCT-1993) to
                                                                                                                                                                                                                                                                                 SEQUENCE FROM
STRAIN-MADRID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=S288C / AB972;
Johnston M., Andrews S.,
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01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 41.7 KDA PROTEIN IN SFP1-CTR3 INTERGENIC REGION
YLR405W OR L8084.2.
                                                                                                                                                    STRAIN-MADRID
                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                             Rickettsiaceae; Rickettsieae; NCBI_TaxID=782;
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Pfam; PF01207; UPF00:
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367 AA; 4
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eae; Rickettsia
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                subdivision; Rickettsiales;
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ATP6_MAIZE
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Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                       Powey. R.E., Levings C.S. III, Timothy D.H.;

"Nucleotide sequence of ATPASE subunit 6 gene of maize mitochondria."

Plant Physiol. 79:914-919 (1985).

-I. FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A
DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE.

-I. SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC

CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE

SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)

HAS THREE MAIN SUBUNITS: A, B AND C.

I. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-I. SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mitochondria.";
nature 396:133-140(1998).
-i- FUNCTION: PROTEIN S7 BINDS SPECIFICALLY TO PART OF THE 3' EN
-i- FUNCTION: PROTEIN S7 BINDS SPECIFICALLY TO PART OF THE 3' EN
-i- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS
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Magnoliophyta; Liliopsida;
Andropogoneae; Zea.
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01-AUG-1988 (Rel. 08, Last sequ
01-NOV-1997 (Rel. 35, Last anno
ATP SYNTHASE A CHAIN (EC 3.6.1
             EMBL; M16223; PIR; JN0042; F
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01-AUG-1988
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PROSITE; PS00052; RIBOSOMAL_S7; 1.
Ribosomal protein; rRNA-binding,
SEQUENCE 160 AA; 18309 MW; 5C66702A37F41761 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4577;
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                                                                                                            non-profit institutions as long
                                                             email to license@isb-sib.ch).
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(EC 3.6.1.34) (PROTEIN
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Best Local
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Interpro; IPR000568; -.
Pfam; PP00119; ATP-Synt.A; 1.
PRINTS; PR00123; ATPASEA,
PROSITE; PS00449; ATPASEA; 1.
PROSITE; PS00449; ATPASEA; 1.
Hydrogen ion transport; CF(0); M
SEQUENCE 291 AA; 31758 MW; 9
                                                                                                                                                                                                                                                                                                                                     MEDLINE-9295987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harri
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harri
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davles R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston
Taylor K., Whitehead S., Barrell B.G.,
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                              TubercuList; Rv1760;
Hypothetical protein.
SEQUENCE 502 AA; 5
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                                                                                                                                                                                                                                       use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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NFQIRHHL 119
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an email to license@isb-sib.ch).
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Pred. No. 37;
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RESULT 14 AMPN_LACHE

Query Match Best Local

6, Similarity

Conservative

Mismatches

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STRAIN=53//;
MEDLINE=95154667; PubMed=7851/5,
Varmanen P., Vesanto E., Steele J.L., Palva A.;
Varmanen P., Vesanto E., Steele J.L., Palva A.;
"Characterization and expression of the pepN gene encoding a general serious of the pepN gene encoding a general minopeptidase from Lactobacillus helveticus.";
FEMS Microbiol. Lett. 124:315-320(1994).
FEMS Microbiol. Lett. 124:315-320(1994)
-i- FUNCTION: AMINOPEPTIDASE N IS INVOLVED IN THE DEGRADATION OF TUNCTION: AMINOPEPTIDES GENERATED BY PROTEIN BREAKDOWN DURING TO NUTRIENT STARVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996
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01-OCT-1996 (Rel. 34, Last sequence update)
01-WOV-1997 (Rel. 35, Last annotation update)
AMINOPEPTIDASE N (EC.3.4.11.2) (LYSYL AMINOPEPTIDASE) (LYS-AP)
                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01433; Peptidase_M1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for con
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293
312
376
39
342
445
496
527
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license agreement (See http://www.isb-sib.ch/announce/
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  50.0%;
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                                                                                        ME.
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ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

PROTON DONOR (POTENTIAL).

F -> I (IN REF. 2).

L -> F (IN REF. 2).

S -> A (IN REF. 2).

K -> R (IN REF. 2).

S -> N (IN REF. 2).

L -> L (IN REF. 2).
Score 38;
Pred. No.
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                        Length 844;
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ID UL70_MCMVS STANDARD; PRT; 964 AA.

AC Q69153;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HELICASE/PRIMASE COMPLEX PROTEIN (PROBABLE DNA REPLICATION PROTEIN UL70).
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Search completed: August Job time: 701 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDILINE-96082764; PubMed=7483291;

Messerle M., Rapp M., Lucin P., Koszinowski U.H.;

"Characterization of a conserved gene block in the murine
cytomegalovirus genome.";

Virus Genes 10:73-80(1995).

-!- FUNCTION: INVOLVED IN DNA REPLICATION (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL52,

EHV-1 7, EBV BSLF1, HVS-1 56, VZV 6, HCMV AND MCMV UL70.
                                                                                                                                                                                                                                                                      EMBL; L07319; AAA96665.1; -. Helicase; DNA replication. SEQUENCE 964 AA; 109704 MV
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Muromegalovirus.
NCBI_TaxID-10367;
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                    9, 2001, 20:36:52
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Post-processing: Minimum Match 0%
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Listing first 45 s
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19.758 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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O9FC35;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE DELTA FATTY ACID DESATURASE.
SC4G1.14C.
                                                                                                                                                                                                                                                                                                     Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.; Kinashi H., Hopwood D.A.; "A set of ordered cosmids and a detailed genetic and physical map the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996); EMBL; AL391039; CRC01.546.1; -." EMBL; AL391039; CRC01.546.1; -." SEQUENCE 347 AA; 37990 MW; 1201E2D716CB46419 CRC64;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

NCBI_TaxID-1902;
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STRAIN-A3(2);
Cerdeno A.M., Parkhill J., B
Submitted (AUG-2000) to the
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Pred. No. 2.3e-05;
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GGLNYQIEHHLFP

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Xing L., Li M., Liu L., Hu G., Zhang L.; "Cloning and sequence analysis of the conserved region of fatty acid desaturase gene from Mortierella alpina."; submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF307942; AAG45094.1; -.
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Q9F2M3;
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Xing L., Liu M., Liu G.;
Xing L., Liu M., Hu G.;
Xing L., Liu M., Hu G.;
Cloning and sequence analysis of the conserved region fatty acid desaturase gene from Mortierella alpina.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
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PROSITE; PS50255; CYTOCHROME_B5_2; 1.
PROSITE; PS00213; LIPOCALIN; UNKNOWN.
SEQUENCE 443 AA; 51740 MW; 9513CF
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Wapier J.A., Hey S.J., Lacey D.J., Shewry P.R.;
"Identification of a Caenorhabditts elegans Delta6-fatty-acid-
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SEQUENCE
                   investigating biology.";
Science 282:2012-2018(1998).
EMBL; AF114440; AAD13294.1;
EMBL; AF078796; AAC95143.1;
EMBL; Z81122; CAB61031.1; -.
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Eukaryota; Metazoa; Nem
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EMBL; 270271; CAA94233.2; -.
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Q9UVY3;
01-MAY-2000
01-MAY-2000
01-MAR-2001
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Q9UVV3;
01-MAY-2000.(TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DELTA-6 FATTY ACID DESATURASE.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-MAR-2001 (TrEMBLrel. 16, Last annotation
DELTA-6 FATTY ACID DESATURASE.
Mortierella_alpina.
                                                                                 MEDLINE-99406036; PubMed=10478922;
Huang Y.S., Chaudhary S., Thurmond J.M., Bobik E.G. Jr., Yuar
Chan G.M., Kirchner S.J., Mukerji P., Knutzon D.S.;
"Cloning of deltal2- and delta6-desaturases from Mortierella
and recombinant production of gamma-linolenic acid in Sacchar
   cerevisiae.";
Lipids 34:649-659(1999)
-!- SIMILARITY: TO CYTO
                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=ATCC32221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPRO01199; -..
Pfam: PF00173; heme_1; 1.
PROSITE; PS00191; CYTOCHROME_B5_1;
PROSITE; PS50255; CYTOCHROME_B5_2;
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Sakuradani E., Kobayashi M., Shimizu S.;
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=64518;
                                                                                                                                                                                                                                                                                                                                                                          Mortierella
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
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Pred.
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Pred. No.
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                                                        Xing L., Li M., Liu L., Hu G., Zhang L.;
"Expression of Mortierella alpina delta 6-fatt
in Saccharomyce cerevisiae.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ
EMBL; AF307940; AAG45092.1;
SEQUENCE 457 AA; 51885 MW; 4BOACODD15D19DA
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01-MAR-2001 (TIEMBLIE1 16, La
01-MAR-2001 (TIEMBLIE1 16, La
DELTA 6-FATTY ACID DESATURASE.
Mortierella alpina.
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Junwu Xitong 0:0-0(2001).
EMBL; AF306634; AAG38104.1; -.
SEQUENCE 457 AA; 51772 MW; 86
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PROSITE; PS00191; CYTOCHROME_B5_1; UNKNOWN_1
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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HSSP; P04166; 1B5M.
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Pred. No. 3.1e-05;
Mismatches 0;
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Oliver K., Harris D.;
Oliver K., Harris D.;
"A set of ordered cosmids and a detailed genetic and
"A set of ordered cosmids and a detailed genetic and
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databas
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99X8W4;

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01-NOV-1999 (TrEMBLrel. 12,

01-NOV-1999 (TrEMBLrel. 12,
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Barrell B.
Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. [3]
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Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Streptomycineae; Stre
ACHINGMICELITAXID=1902;
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01-OCT-2000 (TrEMBLrel. 15,
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01-MAR-2001 (TrEMBLrel. 16,
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EMBL; AL388652; CAB94021.1; -.
SEQUENCE 428 AA; 49418 MW; D6C
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Eukaryota; Euglenozoa;
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"The Delta8 desaturase of Euglena gracilis: an alternate pathway for synthesis of 20-carbon polyunsaturated fatty acids."; Arch. Blochem. Blophys. 365:307-316(1999).
EMBL; AF139720; AAD45877.1; -
InterPro: IPR001199; -
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
SEQUENCE 419 AA; 48457 MW; C2D8EDD092F27FR2 CRC64.
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01-MAY-2000 (TremBI
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DELTA8 FATTY ACID I
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-MAR-2001 (TrEMBLrel. 16, Last annotation
DELTA 6-FATTY ACID DESATURASE.
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"A set of ordered cosmids and a detailed genetic and physical map the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; ALO78610; CAB44485.1: -
SEQUENCE 345 AA; 38022 MW; 1C938614F662DC3A CRC64;
                                                                                                                                           Ceratodon purpureus (Moss).
Eukaryota; Viridiplantae; Embryophyta;
Dicranidae; Dicranales; Ditrichaceae; (
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Eukaryota; Euglenozoa;
CCBI_TaxID=3039;
    MEDLINE=20307617; PubMed=10848999; Sperling P., Lee M., Girke T., Zae
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STRAIN=A3(2);
MEDLINE=97(000351; PubMed=8843436;
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STRAIN-WT3; TISSUE-PROTONEMATA;
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1 Similarity 92.3%;
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(; 48457 MW; C2D8EDD092F27EB2 CRC64;
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Ceratodon.
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C STRAIN-HEBW. B. S. G.;

X MEDLINE-98416756; PubMed-9744093;

X MEDLINE-98416756; PubMed-9744093;

X MEDLINE-98416756; PubMed-9744093;

Y identification of a novel delta 6-acyl-group desaturase by "Identification in Physcomitrella patens.";

T gene disruption in Physcomitrella patens.";

L Plant J. 15:39-48(1998).

L Plant J. 15:39-48(1998).

C -!- SIMILARITY: TO CYTOCHROME B5 DOMAIN.

R EMBL; AJ222981; CAA11033.1; -.

R EMBL; AJ222980; CAA11032.1; -.

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SEQUENCE
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Eukaryota; Viridiplantae; Embryophyta
Funariidae; Funariales; Funariaceae;
NCBI_TaxID=3218;
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Pfam; PF00173; heme_1; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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SEQUENCE 520 AA; 59160 MW; 5A9332EECC153439 CRC64;
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Pfam; PF00173; heme_1;
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EMBL; AJ250735; CAB94993.1;
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Eur. J. Bioche
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Copyright (c) 1993 - 2000 Comp
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sp_unclassified:*
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7.599 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	. 60	80	7	6	U	4	ω	2	1	No.	Result
30	30	30	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	Score	
93.8	93.8	93.8	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Match Length	Query
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RESULT Q9UVY3

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ALIGNMENTS

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Query Match
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                                                                                                                        Xing L., Liu L., Hu G., Zhang L.;

"Cloning and sequence analysis of the conserved region of fatty acid desaturase gene from Mortierella alpina.";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF307942; AAG45094.1; -.

EMBL; AF307941; AAG45093.1; -.

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SEQUENCE 357 AA; 40796 MW; C8D9CE1283BB16B8 CRC64;
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Xing L., Li M., Liu L., Hu G.;

"Cloning and sequence analysis of the conserved region of fatty acid desaturase gene from Mortierella alpina.";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                              Q9HDF4 PRELIMINARY; PRT; 357 AA.
Q9HDF4;
Q1-MAF-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DELTA 6-FATTY ACID DESATURASE (FRAGMENT).
Mortierella alpina.
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae; Mortierella.
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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127 HDFLH
                            1 HDFLH 5
131
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Pred. No. 27;
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Matches 5; Conserv
Query Match
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MEDLINE-99406036; PubMed-10478922;

Huang Y.S., Chaudhary S., Thurmond J.M., Bobik E.G. Jr., Yuan Huang Y.S., Chaudhary S.J., Mukerji P., Knutzon D.S.;

"Chan G.M., Kirchner S.J., Mukerji P., Knutzon Mortierella Chan G.M., First And delta6-desaturases from Mortierella Chango of delta12- and delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delta6-desaturases from Mortierella Chango of delt
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Q9UVY3;
01-MAY-2000
01-MAY-2000
01-MAR-2001
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                               Heme.
SEQUENCE
                                                                                                                         Pfam; PF00173; heme_1; 1.
PROSITE; PS00191; CYTOCHROME_B5_1; PROSITE; PS50255; CYTOCHROME_B5_2;
                                                                                                                                                                                                                             -!- SIMILARITY: TO CYTOCHROME EMBL; AF110510; AAF08685.1; -. HSSP; P04166; 185M.
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Eukaryota; Fungi;
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PROSITE; PS00191; CYTOCHROME_B5_1; UNKNOWN_1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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"Delta 6-Fatty acid desaturase from an ara
Mortierella fungus. Gene cloning and its
fungus, Aspergillus.";
Gene 238:445-453(1999).
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Eukaryota; Fungi;
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                                                                                                                                                                                                        InterPro;
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SEQUENCE
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Q9HEY4;
Q1-mar-2001 (TrembLrel.
                                                                                                                                                                         in Saccharomyce cerevisiae.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ
EMBL; AF307940; AAG45092.1; -.
SEQUENCE 457 AA; 51885 MW; 4B0AC0DD15D19DA
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Q9LEN0
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Eukaryota; Fungi; 2
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EMBL; AF306634; AAG38104.1; -
SEQUENCE 457 AA; 51772 MW;
                                                                                                                                                                                                                                   Xing L.,
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                                                                                                                                                                                                                                                                       NCBI_TaxID=64518;
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Expression of Mortierella alpina delta
n Saccharomyce cerevisiae.";
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delta6-fatty a
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O1-OCT-2000 (TrEMBLrel. 15,
O1-OCT-2000 (TrEMBLrel. 16,
O1-MAR-2001 (TrEMBLrel. 16,
DELTA 6-FATTY ACETYLENASE.
                                                                                                                                                                                                                                                                                                                                                                                                         09LEM9; PRELIMINARY; PRT; 520 AA.
09LEM9; O1-CT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20307617; PubMed-1084999; speriing P., Lee M., Girke T., Zaehringer U., Stymne S., H Speriing P., Lee M., Girke T., Zaehringer U., Stymne S., H Abifunctional delta 6-fatty acyl acetylenase/desaturase moss Ceratodon purpureus. A new member of the cytochrome b superfamily.";
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIL-WT3; TISSUE-PROTONEMATA;
MEDLINE-20307617; PubMed-10848999;
MEDLINE-20307617; PubMed-10848999;
Sperling P. Lee M., Girke T., Zaehringer U., Stymne S., H
"A bifunctional delta 6-fatty acyl acetylenase/desaturase
"Na bifunctional delta 6-fatty acyl acetylenase/desaturase
"One of the cytochrome b
                                                                                                                                                                                                                                                                                                                                                   Ceratodon purpureus (Moss).
Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;
Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
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Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;
Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
NCBI_TaxID=3225;
                                                                                                                                                                                                                                                                                                                                           Dicranidae; Dicranales; NCBI_TaxID=3225;
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STRAIN-WT3; TISSUE-PROTONEMATA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212
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Pfam; PF00173; heme_1;
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                                                 HDFLH
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AJ250735; CAB94993.1; -.
Pro; IPR001199; -.
PF00173; heme_1; 1.
TE; PS50255; CYTOCHROME_B5_2; 1.
NCE 520 AA; 59160 MW; 5A9332EECC153439 CRC64;
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5; Conserv
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15, Last sequence update)
16, Last annotation update)
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Pred. No.
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STRAIN-HEDM. B. S. G.;

STRAIN-HEDM. B. S. G.;

MEDLINE-98416756; PubMed-9744093;

MEDLINE-98416756; PubMed-9744093;

Midentification of a novel delta 6-acyl-group des gene disruption in Physcomitrella patens.";

Plant J. 15:39-48(1998).

-i-SIMILARITY: TO CYTOCHROME B5 DOMAIN.

EMBL; AJ222980; CAA11032.1; -.

EMBL; AJ222980; CAA11032.1; -.

HSSP; P04166; 1BBM.
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P94896;
01-MAY-1997
01-MAY-1997
01-MAR-2001
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Q9ZNW2;
01-MAY-1999
01-MAY-1999
01-MAR-2001
Pfam; PF00205; TPP_enzymes; 1.
PROSITE; PS00187; TPP_ENZYMES;
Flavoprotein; Lysse; Thiamine y
SEQUENCE 560 AA; 61459 MW;
                                                                                "Cloning and sequencing of the gene encoding decarboxylase from Leuconostoc oenos."; FEMS Microbiol. Lett. 145:445-450(1996).
-i- CATALYTIC ACTIVITY: 2-ACETOLACTATE + CO(2-i- CATALYTIC THIAMIN PYROPHOSPHATE.
-i- COFACTOR: THIAMIN PYROPHOSPHATE.
                                                                                                                                                         STRAIN-LO 84.13;
MEDLINE-97132647; PubMed-8978099;
Garmyn D., Monnet C., Martineau B.,
                                                                                                                                                                                                                                                                              01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat
ALPHA-ACETOLACTATE SYNTHASE (EC 4.1.3.18).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Funariidae; Funariales;
NCBI_TaxID=3218;
                                             PYROPHOSPHATE.
EMBL; X93091; CAA63640.1;
InterPro; IPR000399; -.
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pfam; PF00173; heme_1; 1.
pr0SITE; PS50255; CYTOCHROME_B5_2;
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Eukaryota; Viridiplantae; Eml
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                     Oenococcus.
NCBI_TaxID=1247;
                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
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(TrEMBLrel. 10,
(TrEMBLrel. 16,
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pyrophosphate.
CADC2C1C181C0D1A CRC64;
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4.1.3.18).
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Length 560;

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Matches
                   Isogai T., Ota T., Hayashi K., Su
Nishikawa T., Nagai K., Sugano S.
Tanai H., Kimata M., Watanabe M.,
Saito K., Yamamoto J., Wakamatsu
Masuho Y., Kanehori K.;
                                                       (1)
SEQUENCE FROM N.A.
Ota T., Hayashi K.,
Suqano
                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat
CDNA FLJ10619 FIS, CLONE NT2RP2005472.
                                                                                                                                                                                                                                                                                                                                                Jia Y., Cherry J.M.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ
EMBL; U33007; AAA64868.1; -.
SGD; S0002848; DOT1.
SGD; S0002848; DOT1.
SGD; S0002848; DOT1.
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Submitted
 "NEDO human cDNA sequencing Submitted (FEB-2000) to the
                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                 Homo sapiens (Human).
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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D9461.26 OR DOT1.
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Primates;
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Pred. No.
                                         , Sugiyama T., Otsuki T., Suzuki Y.,
o S., Ishibashi T., Fujimori K.,
M., Hiraoka S., Ishii S., Kawai Y.,
                                                                                                          Craniata; Vertebrata; Catarrhini; Hominidae
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Pfam; PF00069; LRERICHRPT.

Pfam; PF000019; LEURICHRPT.

PRINTS; PR00109; TYRKINASE.

PROSITE; PS00107; PROTEIN_KINASE_ATP; UN

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

SMART; SM00221; STYKC; 1.

ATP-binding; Kinase; Transferase; Tyrosi

SEQUENCE 717 AA; 77634 MW; 5CECAC430
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Clones. 7:131-135(2000).
DNA Res. 7:131-135(2000).
EMBL; AB022220; BAB01040.1;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat
SERINE/THREONINE PROTEIN KINASE-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Trachec
Magnoliophyta; eudicotyledons; core eudicots;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-1999)
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Sato S., Nakamura Y.,
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RESULT 15
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Q9QZD4;
Q19QZD4;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DNA REPAIR ENDONUCLEASE XPF.
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 Q9UGA1;
01-MAY-2000
01-MAY-2000
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Endonuclease.
917 AA;
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Genomics 0:0-0(1999).

Genomics 0:0-0(1999).
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Mammalia; Eutheria;
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Eukaryota; Metazoa; (
Mammalia; Eutheria; I
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PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                 SEQUENCE
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7.651 Million cell updates/sec
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447	447	517	458	450	449	449	449	449	2 449	353	2 353	2 326	2 326	284	252	224	2 104	2 76	6 448	6 448	6 448	6 448	6 446	6 253	222	83	422	483	483	448	469	8 462	520
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. elegans fatty	C. elegans delta 5	Arabidopsis thali	Sphingolipid desa	Soybean sphingoli	na sl	B. napus sld1 prot		Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia			Arabidopsis thalia	Protein b51bo with	Desaturase enzyme	Protein d51pu with	turase	Sunflower hypothet	Sunflower HADES pr	Borage delta-6 des	Borage delta-6 des	Borage delta-6-des	A delta-6 desatura	ш.	tei	elta 6 desturas	. gracilis f	. purpureus	C. purpureus delta	Florida bitterbush	Wheat sphingolipid	Corn sphingolipid	C. purpureus delta

ALIGNMENTS

AAW84139 RESULT

AAW84139 standard; Peptide;

355

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AAW84139;

15-FEB-1999

(first entry)

Desaturase enzyme peptide sequence.

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Fatty acid; desaturase; polyunsaturated fatty acid; malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis; cancer; diabetes; eczema; platelet aggregation; vasodilation; cholesterol level; endometriosis; premenstrual syndrome; myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis; acute respiratory syndrome; hypertension; inflammatory skin disorder.
                    Chaudhary S, Thurmond J;
WPI; 1998-594582/50
                                                                                                                                                                          Unidentified
                                                                                     11-APR-1997;
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                                                   (ABBO ) ABBOTT LAB.
(CALJ ) CALGENE LLC.
                              Huang Y,
                                                                                     97US-0834655
                                                                                                          98WO-US07126
                               Knutzon
                               D,
                                Leonard
                                ΑE,
                              Mukerji P;
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RESULT
AAY17751
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Desaturase enzymes, the genes encoding them and their uses
                                                                                         N-PSDB;
                                                                                                                                     WPI; 1999-370905/31
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                                                                                                                                                                                                                                                                                                           (UYBR-)
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fatty acid and for producing a desaturated fatty acid by expressing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            raise and select antibodies (which may be used in immunoassays, and diagnostic tests to detect the presence of (I) in a sample, or to purify (I)) or as a selectable marker for transformation, especially transformations involving plants. (I) can be used to produce gammalinolenic acid (GLA) (and derivatives of it), which is a high value plant fatty acid that is widely used in medicine for the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the
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WPI; 1998-594582/50
                                                                   Chaudhary S, Thurmond J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        myalgic encephalomyelitis; chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cholesterol level; endometriosis; premenstrual syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 malnutrition; inflammation; rheumatoid arthritis; asthma; psc
cancer; diabetes; eczema; platelet aggregation; vasodilation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fatty acid; delta-6 desaturase; polyunsaturated fatty acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A delta-6 desaturase enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treated with GLA and OTA include eczema, mastalgia, atherosclerosis, hypercholesterolaemia, coronary disease, diabetic neuropathy, viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or deficiencies in metabolites derived in vivo from GLA, such as octadecatetraenoic acid (OTA) and eicosanoids. Disorders that may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 1; 44pp; English
                                                                                                                                                             (ABBO ) ABBOTT LAB. (CALJ ) CALGENE LLC.
                                                                                                                                                                                                                                                              11-APR-1997;
                                                                                                                                                                                                                                                                                                                              10-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                              22-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mortierella alpina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW84137 standard; Protein; 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cleaving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           compositions for treating disorders associated with deficiencies in GLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 wwkdkhnthh 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 WWKDKHNTHH 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   respiratory syndrome; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNA molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          443 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                          Huang Y,
                                                                                                                                                                                                                                                              97US-0834655
                                                                                                                                                                                                                                                                                                                              98WO-US07126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                    Knutzon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 73; DB 20;
Pred. No. 0.00099;
                                                                                       D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fatigue; AIDS; multiple sclerosis;
                                                                                                    Leonard AE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 443;
                                                                                                    Mukerji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to purify
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ទ
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N-PSDB; AAV63624

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC the invention. The specification describes methods for desaturating a confirmation of the producing a desaturated fatty acid by expressing concerns the introduces a double bond carbons 6 and 7 from the carboxyl end of a fatty acid molecule. The enzyme can be used for desaturating fatty cards. The enzyme can be used to produce polyunsaturated fatty acids, which can be used for treating malnutrition, in pharmaceutical compositions, in cosmetics or in animal feed. The polyunsaturated fatty cards can be used for treating e.g. restenosis after angioplasty, compositions, in cosmetics or in animal feed. The polyunsaturated fatty cards can be used for treating e.g. restenosis after angioplasty, corresponding to the composition, rheumatoid arthritis, asthma, psoriasis, cancer, diabetes corrected are reduce blood pressure. They can also be used to inhibit confidence blood pressure. They can also be used to inhibit proliferation of vessel wall smooth muscle and fibrous tissue, creduce or prevent gastro-intestinal bleeding and other side effects caused by non-steroidal anti-inflammatory drugs, prevent or treat candometriosis and premenstrual syndrome, treat myalgic encephalomyelitis and chronic fatigue after viral infections, treat AIDS, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated fatty acid desaturase enzymes - used for the production of polyunsaturated fatty acids for use in, e.g. pharmaceutical compositions, nutritional compositions, cosmetics or animal feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW95504 standard; peptide; 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                  11-APR-1997;
11-APR-1997;
                                                                                                                                                                                                                        Mortierella alpina
                                                                                                                                                                                                                                                                                        polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic; stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula; dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;
                                                                                                                                                                                                                                                                                                                                                Delta
                                                                                                                                                                                                                                                                                                                                                                                Mortierella alpina delta 6 desaturase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW95504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           desaturase enzyme.
(ABBO ) ABBOTT
                                                                                    24-OCT-1997;
                                                                                                                      10-APR-1998;
                                                                                                                                                                                                                                                                             rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sclerosis, acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 WWKDKHNTHH 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 desaturase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig 3A-E;
                                                                                                                                                                                                                                                            cosmetic;
                                                                                                                                                                                                                                                                          arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence represents a Mortierella alpina fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                 97US-0956985.
97US-0833610.
97US-0834033.
97US-0834655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yme. The enzyme sequence is used in t
The specification describes methods
                                                                                                                      98WO-US07421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                respiratory syndrome, hypertension and inflammatory skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165pp; English
                                                                                                                                                                                                                                                            animal
                                                                                                                                                                                                                                                                                                                                            recombinant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                            feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 73; DB 19
Pred. No. 0.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                            fatty acid desaturase; FAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                            PUFA; oil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of.
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RESULT
AAW85121
ID AAW8
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                     cancer; diabetes; eczema; platelet aggregation; vasodilation;
cholesterol level; endometriosis; premenstrual syndrome;
myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
acute respiratory syndrome; hypertension; inflammatory skin disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dietary supplements or substitutes, for use in humans or animals; (111) for treating disorders associated with inadequate consumption or production of PUFA (or their metabolites such as prostaglandins), e.g. restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis, psoriasis, osteoporosis, cancer, eczema, diabetes; (1v) as cosmetics, and (v) as animal feeds. Fragments of the DNA are used as probes to isolate related coding sequences. Recombinant plants can produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields of the produce high yields yields of the produce high yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yields yie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleotide sequences (AAX00889 to AAX00891) encoding M. alpina delta delta 12 and delta 5 desaturases (AAW95504 to AAW95506) respectively, coupled to an expression control sequence functional in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid construct able to express fatty acid desaturase in plants - useful in human or animal nutrition, as cosmetics and therapeutically, e.g. for restenosis, cancer and diabetes
                                                                                                                                                                                                                                                                       Fatty acid; delta-6 desaturase; polyunsaturated fatty acid;
malnutrition; inflammation; rheumatoid arthritis; asthma; p
                                                                                                                                                                                                                                                                                                                                                   A delta-6 desaturase enzyme amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Fig 3A-E; 210pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-080739/07.
N-PSDB; AAX00889.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thurmond J;
                                                                                                                                                                                                                                                                                                                                                                                                     11-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW85121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW85121 standard; Protein; 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plants can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant plant cells containing at least one DNA encoding
                                                                       WO9846765-A1
                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CALJ ) CALGENE LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 WWKDKHNTHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    one similar to that with e.g. fish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         since new pathways can be created and unwanted ones suppressed. s can be engineered to express oils of particular PUFA composition, one similar to that in human milk, and product recovery is simpler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e.g. fish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΑA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mortierella alpina delta 6 desaturase. The invention sic acid construct that contains at least one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 73; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Knutzon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 457;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                       psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a M. alpina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           are
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a fatty acid delta-6 desaturase enzyme. The specification describes methods for desaturating a fatty acid and for producing a desaturated fatty acid by expressing increased levels o a desaturase. The present desaturase is an enzyme which introduces a double bond carbons 6 and 7 from the carboxyl end of a fatty acid molecule. The enzyme can be used for desaturating fatty acids. The enzyme can be used for desaturated fatty acids, which can be used for treating malnutrition, in pharmaceutical compositions, in cosmetics or in animal feed. The polyunsaturated fatty acids can be used for treating e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis, asthma, psoriasis, cancer, diabetes or eczema or reduce hand arthritis, asthma, psoriasis, cancer, diabetes or eczema or reduce hand arthritis, asthma, psoriasis, cancer, diabetes or eczema or reduce hand arthritis, asthma, psoriasis, cancer, diabetes or eczema or reduce hand arthritis, asthma, psoriasis, cancer, diabetes or eczema or reduce hand arthritis, asthma psoriasis, cancer, diabetes or eczema or reduce hand arthritis asthma psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or reduce blood pressure. They can also be used to inhibit platelet aggregation, cause vasodilation, lower cholesterol levels, inhibit proliferation of vessel wall smooth muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding and other side effects caused by non-steroidal anti-inflammatory drugs, prevent or treat endometriosis and premenstrual syndrome, treat myslyic encephalomyelitis and chronic fatigue after viral infections, treat AIDS, multiple
                                                                                                                                                                     transgenic insect cell; polyunsaturated long chain fatty acid; antiinflammatory; antirheumatic; antiasthmatic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ABBO )
(CALJ )
                       Misc-difference
                                                                             Mortierella alpina
                                                                                                                                  anti-HIV; neuroprotective; hypotensive; nephrotropic; vasodilator;
                                                                                                                                                     osteopathic; cytostatic; antidiabetic; dermatological;
                                                                                                                                                                                                          delta-6 desaturase; gamma-linolenic acid;
                                                                                                                                                                                                                                                                                      10-AUG-2000
                                                                                                                                                                                                                                                                                                                           AAY92599
                                                                                                                                                                                                                                                                                                                                                            AAY92599 standard; Protein; 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used, e.g. for treating cancer, as foods,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-009334/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chaudhary S, Thurmond J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sclerosis, acute respiratory syndrome, hypertension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 wwkdkhnthh 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 WWKDKHNTHH 10
                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid encoding delta5 and other desaturase enzymes ful in production of oils of increased arachidonic acid co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABBOTT LAB.
CALGENE LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                 delta-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huang Y,
                                                                                                                  vasotropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₿
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                       Location/Qualifiers 172..176
   /label= histidine_box
                                                                                                                                                                                                                                                 fatty acid desaturase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95-96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 73; DB 20
Pred. No. 0.001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 20;
                                                                                                                                                                                                          biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   animal feeds and cosmetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 457;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and inflammatory skin
                                                                                                                                                     gynecological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      content,
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                                                                                                                                                                                                                                                                                                                                                                                             alpha-linolenic acid to stearidonic acid. Transgenic insect cells comprising a nucleotide sequence which encodes a polypeptide comprising corresidues 50-53, 39-43, 172-176, 204-213, or 390-402 of delta-5 cc desaturase (AAY92599) or comprising delta-12 desaturase (AAY92600) are colaimed. Oil and fatty acids (especially gamma-linolenic acid) isolated from the recombinant insect cells are also claimed. Production of colling the recombinant insect cells are also claimed. Production of collyunsaturated long chain fatty acids (PUFAs) in insect cells has many collyunsaturated to external variable fluctuations, and can easily be maintained and manipulated. The oils are used in pharmaceutical compositions, infant formulas, dietary supplements or substitutes, and cosmetics (all claimed). The PUFA supplements have antiinflammatory, antidiabetic, dermatological, anti-HTV, neuroprotective, bypotensive, nephrotropic, vasodilator, antiaggregant and vasotropic
                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel transgenic insect cells comprising a nucleotide sequences which encode delta-6-desaturase or delta-12- desaturase, useful for producing poly-unsaturated long chain fatty acids, e.g. arachidonic acid
                           Polyunsaturated fatty acid; fungus; delta6-desaturase; animal feed;
                                                         Fungal delta6-desaturase protein sequence.
                                                                                      28-MAR-2000
                                                                                                                   AAY56045;
                                                                                                                                              AAY56045 standard; Protein; 457
                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 145-146; 170pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                     activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200020602-A2
                                                                                                                                                                                                                        204 wwkdkhnthh
                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                   1 WWKDKHNTHH 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fatty acid desaturases are able to catalyse the conversion of oleic to inoleic acid, linoleic acid to gamma-linolenic acid or of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-328935/28
                                                                                                                                                                                                                                                                                 l Similarity
10; Conser
                                                                                                                                                                                                                                                                                                                                                         457
            animal; malnutrition;
                                                                                                                                                                                                                                                                            100.0%;
ilarity 100.0%;
Conservative 0
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                                                                                    (first entry)
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                                                                                                                                                                                                                         213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "conserved 395..399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
209..21
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/note= "conserved amo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= histidine
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                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                             Score 73; DB 21
Pred. No. 0.001;
                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                             21;
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                                                                                                                                                                                                                                                                                                           Length 457;
                                                                                                                                                                                                                                                                                 Indels
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transgenic

biosynthesis

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RESULT
AABJA684
ID AABS
XX ABS
AC AABS
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XX 30-4
XX 601
E Amir
XX del!
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                            delta6 desaturase; desaturase gene; elongase gene; fatty a eicosanoid; nutrition; infant formula; dietary supplement; dietary substitute; animal feed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence corresponds to a fungal delta6-desaturase whose coding sequence is an example of a nucleic acid sequence used to transform the cells. The essential FAs obtained can be used in nutritional formulations or animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprising animal cells producing essential fatty acids (FAs). The animal cells are produced by transforming cells, e.g. embryonic stem cells, with nucleic acid encoding heterologous enzymes involved in fatty acid, e.g. long chain or polyunsaturated fatty acid (PFA) biosynthesis. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          downstream products such as leukotrienes, thromboxanes, arachidonic acid, elcosapentaenoic acid or docosahexaenoic acid. The products can also be used in cell culture. The animal or milk fat produced can be administered
               11-JUL-2000; 2000WO-US19011.
                                                                                                                                                                                                                                                                              AAB31684 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   products can also be used for producing transgenic animals which used for producing essential FAs which can be used for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 9;
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N-PSDB; AAZ47129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                            18-JAN-2001
                                                                                                  Mortierella alpina.
                                                                                                                                                                                      Amino acid sequence of a fungal delta6 desaturase
                                                                                                                                                                                                                      30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   feed formulations. The long chain PFAs can be used in nutritional formulations, cosmetic formulations or animal feed formulations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kopchick JJ, Kelder B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (OHIS ) UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                1 WWKDKHNTHH 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treat malnutrition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to a method of generating novel compositions
                                                                                                                                                                                                                                                                                                                                                     wwkdkhnthh
                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ng essential fatty acids and long-chain for use in nutritional, animal feed and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     457
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                    (first
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                                                                                                                                                                                                                                                                              Protein; 457
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 457;
                                                                                                                                                            fatty acid;
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RESULT
AAY51353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               formulae, e.g. infant formula, dietary supplements or dietary substitutes for both humans and animals. The compositions are also useful in cosmetic or animal feed formulations. Furthermore, the compositions may also be used as fat free media or as research reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synthesising essential fatty acids, their derivatives or downstream products, as well as altered levels of long-chain polyunsaturated fatty acids and eicosanoids. The compositions are useful in nutritional
                                                                                                                                                                                                                                                                                                                                                                                                                                                              transgenic plant; crop plant; delta-8-unsaturated long-chain base; tolerance; resistance; soil salinity; ion stress; toxicity; drough cold; frost; phytopathogenic microorganism; flowering time; cosmet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New compositions comprising cells
elongases, for synthesizing essent
polyunaaturated fatty acids, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          produce animal cells expressing a desaturase gene and/or an elongase gene. Compositions comprising cells of the invention are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The
                                             WPI; 2000-127549/12
                                                                                           Heinz E,
                                                                                                                                                                                                                                                                                           30-DEC-1999
                                                                                                                                                                                                                                                                                                                                           DE19828850-A1
                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sphingolipid desaturase; sldl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein b5cae with delta6 fatty acid desaturase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY51353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-182622/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-JUL-1999;
                                                                                                                                         (GVSE-)
                                                                                                                                                                                            27-JUN-1998;
                                                                                                                                                                                                                                          27-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kopchick JJ,

    WWKDKHNTHH

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tormulations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                            GVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF25234.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; Protein; 473
                                                                                         Zaehringer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      457
                                                                                                                                            GES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence represents a delta6 desaturase.
                                                                                                                                                                                                                                                                                                                                                                                                                                       phytopathogenic microorganism;
al; food; chemical raw material
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kelder
                                                                                                                                                                                            98DE-1028850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0351525
                                                                                                                                                                                                                                          98DE-1028850
                                                                                                                                         ERWERB & VERW LANDWIRTSCHAFTLICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; 93pp;
                                                                                           ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          was used to trasfect mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.0%;
                                                                                           Schmidt H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cells that express desaturases essential fatty acids or long-c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 73;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sphingobase; ceramide; capnoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in nutritional,
                                                                                           Sperling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cosmetic or animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The desaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   long-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 drought;
cosmetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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New sphingolipid desaturase that selectively introduces double bond

into sphingolipids and

capnoids

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RESULT :
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Best Local S
Matches 10
This invention describes a novel sphingolipid desaturase that selectively introduces a double bond into the sphingobase of the ceramide residue of
                                                                                                                                                                                                                                                                                                                                                                                                    Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid; transgenic plant; crop plant; delta-8-unsaturated long-chain base; tolerance; resistance; soil salinity; ion stress; toxicity; drought; cold; frost; phytopathogenic microorganism; flowering time; cosmetic; pharmaceutical; food; chemical raw material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exclude production of delta-8-unsaturated bases, to increase tolerance or resistance to soil salinity, ion stress or toxicity, drought, wet conditions, cold or frost and/or phytopathogenic microorganisms, or to alter size growth and flowering time. Cells, transgenic organisms or plants containing the DNA sequence can be used to produce sphingolipids and capnoids with unsaturated sphingobases. The sphingolipids or capnoids can be used in cosmetics, pharmaceuticals and foods and as chemical raw materials. This sequence represents a protein which has delta6 fatty acid desaturase activity which is described in the method of the invention.
                                                     Disclosure; Fig 16; 62pp;
                                                                                       into
                                                                                                                                         WPI; 2000-127549/12
                                                                                                                                                                      Heinz E,
                                                                                                                                                                                                                                                                        27-JUN-1998;
                                                                                                                                                                                                                                                                                                          30-DEC-1999.
                                                                                                                                                                                                                                                                                                                                         DE19828850-A1
                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY51354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY51354 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     introduces a double bond into the sphingobase of the ceramide residue of sphingolipids and capnoids. A DNA sequence encoding the sphingolipid desaturase, or a vector containing the DNA sequence, can be used to produce transgenic plants, especially crop plants, with an increased or decreased delta-8-unsaturated long-chain base content or an altered delta-8-unsaturated long-chain base cis/trans ratio, especially to
                                                                                                                                                                                                       (GVSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein b5pp with delta6 fatty acid desaturase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       compensate for a delta-8-unsaturated long-chain base deficiency,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        introduces a double bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 WWKDKHNTHH 10
                                                                                     sphingolipid desaturase that selectively introduces double bond sphingolipids and capnoids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                        GVS GES
                                                                                                                                                                      Zaehringer U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            473 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                         98DE-1028850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       describes a novel sphingolipid desaturase that selectively
                                                                                                                                                                                                       ERWERB & VERW LANDWIRTSCHAFTLICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38-39;
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                                                                                                                                                                      Schmidt H,
                                                     German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Pred. No. 0.0011;
Mismatches 0
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                                                                                                                                                                      Sperling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                decreased delta-8-unsaturated long-chain base content or an altered delta-8-unsaturated long-chain base cis/trans ratio, especially to compensate for a delta-8-unsaturated long-chain base deficiency, to exclude production of delta-8-unsaturated bases, to increase tolerance or resistance to soil salinity, ion stress or toxicity, drought, wet conditions, cold or frost and/or phytopathogenic microorganisms, or to alter size growth and flowering time. Cells, transgenic organisms or plants containing the DNA sequence can be used to produce sphingolipids and capnoids with unsaturated sphingobases. The sphingolipids or capnoids can be used in cosmetics, pharmaceuticals and foods and as chemical raw materials. This sequence represents a protein which has delta6 fatty acid desaturase activity which is described in the method of the invention.
This invention describes a novel preparation of unsaturated fatty acids (I) by introducing into an organism at least one isolated nucleic acid (II) that encodes a polypeptide (III) with Delta6-desaturase activity. Organisms that contain at least I wt.% (I), on total fatty acid content, are then selected. (II) is selected from: (a) a 2012 bp sequence (S1), defined in the specification, or its equivalents within the degeneracy of the genetic code; or (b) derivatives of the sequence of (a) that encode a
                                                                                                                                                                                      Production of unsaturated fatty acids, useful e.g. in nutrition, cosmetics or pharmaceuticals, in organisms transformed with Physcomitrella patens delta-6-desaturase nucleic acid -
                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-1999;
30-JUN-2000;
                                                                                                                                                    Claim 1c; Page 41-43;
                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                 WPI; 2001-123117/13
                                                                                                                                                                                                                                                                                                                    Heinz E,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200102591-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Physcomitrella patens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agricultural chemical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Delta6-desaturase; unsaturated fatty acid; transgenic; oil; lipid; fatty acid; human nutrition; animal nutrition; cosmetic; pharmaceu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P. patens delta6-desaturase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB46810;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sphingolipids and capnoids. A DNA sequence encoding the sphingolipid desaturase, or a vector containing the DNA sequence, can be used to
                                                                                                                                                                                                                                                                                                                                                        (BADI ) BASF AG.
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                                                                                                                                                                                                                                                                AAF26040.
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                                                                                                                                                                                                                                                                                                                    Girke T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  525 AA;
                                                                                                                                                                                                                                                                                                                                                                                            2000DE-1030976
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                                                                                                                                                                                                                                                                                                                   Scheffler J,
                                                                                                                                               49pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.04
1; Mismatches
                                                                                                                                                    German.
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                                                                                                                                                                                                                                                                                                                    Da Costa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .041;
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                                                                                                                                                                                                                                                                                                                    Silva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 525;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pharmaceutical;
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degeneracy of

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RESULT 1
AAB46440
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Best Local
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This invention describes a novel isolated nucleic acid (I) encoding polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase activity. The invention also describes (a) amino acid sequences encoded by (I); (b) an expression cassette (EC) containing (I) linked to one or more regulatory sequences; (c) a vector containing (I) and EC; (d) organisms containing (I), EC or the vectors of (C); (e) preparation of unsaturated fatty acids (A) or triglycerides (TG) with increased content of (A) by introducing (I) or EC into an oil-producing organism; (f) production of (A) or TG by using (Ia); and (h) (A) and TG produced by method (g). (I) are used to produce transgenic plants (or other organisms) that produce oils or triglycerides (TG) with increased content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  525 amino acid polypeptide ($2), defined in the specification, or a polypeptide with at least 50% homology with ($2) and practically the same enzymatic activity. The invention also describes (1) transgenic organisms that contain (II); and (2) oils, lipids and fatty acids produced by the new method. The oils, lipids and fatty acids produced by the transformed organisms are used in human or animal nutrition, cosmetics, pharmaceuticals and agricultural chemicals. (III) can also be used, in vitro, for increasing the (I) content of triglycerides. The transgenic organisms have increased contents of (I), or of (I)-containing triglycerides, particularly of gamma-linolenic acid.
                                                                                                                                                                                                                                                        Nucleic acid encoding producing plant oils v
                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1999;
22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C. purpureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB46440 standard; Protein;
                                                                                                                                                                                                          Example 7; Page 57-59; 69pp; German.
                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                       Heinz E,
                                                                                                                                                                                                                                                                                                                                                                                      (BADI ) BASF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ceratodon purpureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB46440
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286 wwkekhnlhh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity les 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 WWKDKHNTHH 10
                                                                                                                                                                                                                                                                                                           AAF25734
                                                                                                                                                                                                                                                                                                                                                     Stymne S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plant; plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          delta6-acetylenase/delta6-desaturase SEQ
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99DE-1062409
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                                                                                                                                                                                                                                                          g delta6-acetylenase
with increased conte
                                                                                                                                                                                                                                                                                                                                                       Lee
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Pred. No. 0.041;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                       Girke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          triglyceride; nutrition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                       Т,
                                                                                                                                                                                                                                                        enase or desaturase, useful for content of unsaturated fatty acids
                                                                                                                                                                                                                                                                                                                                                     Sperling
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                                                                                                                                                                                                                                                                                                                                                       Zaehringer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            animal feed;
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Qy

1 WWKDKHNTHH

Query Match Best Local Matches

Similarity 8; Conser

80.8%;

Score 59; DB 2 Pred. No. 0.15;

21;

Length 462;

Conservative

0,

Mismatches

2

·Indels

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Gaps

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Query Match
Best Local Similarity
Thehes 8; Conserve
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                      The present sequence is a sphingolipid desaturase from clone cdelc.pk001.08:fis isolated from corn developing embryo cDNA library, cdelc. The present sequence is useful for producing transgenic plants having altered levels of sphingolipid desaturase which in turn would alter the fatty acid composition. The enzyme is also useful for producing polyclonal or monoclonal antibodies. The polynucleotide is useful as primer or probe for screening cDNA libraries to isolate desired full-length cDNA clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of unsaturated fatty acids (A) and to isolate related sequences by homology screening. (A), or TG containing them, are useful in human nutrition (e.g. infant foods), animal feeds, pharmaceuticals and cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can be used to suppress expression of (II), resulting in oils with increased content of saturated fatty acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corn; sphingolipid desaturase;
                                                                                                                                      Claim 10; Page 42-43; 57pp; English
                                                                                                                                                               Polynucleotide encoding detransgenic plants and for useful for screening cDNA
                                                                                                                                                                                                                                  WPI; 2000-412336/35
                                                                                                                                                                                                                                                         Cahoon
                                                                                                                                                                                                                                                                                                            03-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corn sphingolipid desaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY71552 standard; Protein; 462 AA
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                       transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 wwktkhnlhh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13
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                                                                                                                                                                                                                                                         EB,
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 462
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A
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                                                                                                                                                                                                                                                                                                            98US-0110784.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       fatty acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.2%;
                                                                                                                                                                 delta-6 desaturase enzyme useful for or producing antibodies specific to when the expression libraries -
                                                                                                                                                                                                                                                         Hitz WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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Pred. No.
                                                                                                                                                                                                                                                                                   င္ပ
                                                                                                                                                                                                                                                                                                                                                                                                                                                     membrane-bound desaturase;
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                                                                                                                                                                                                                                                         Kinney
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                                                                                                                                                                              or producing which is
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망

204 wwkcnhnthh 213

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RESULT
AAY7155
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Best Local
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transgenic plant; fatty acid; membrane-bound desaturase.
             Florida bitterbush;
                                   Florida bitterbush delta-6 fatty acid desaturase.
                                                              12-OCT-2000
                                                                                                          AAY71551 standard; Protein; 448 AA.
                                                                                                                              55
                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                            seedling root cDNA library, wrel.
The present sequence is useful for producing transgenic plants having altered levels of sphingolipid desaturase which in turn would alter the fatty acid composition. The enzyme is also useful for producing polyclonal or monoclonal antibodies. The polynucleotide is useful as primer or probe for screening cDNA libraries to isolate desired full-length cDNA clones.
                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a sphingolipid desaturase from clone wre1.pk0004.c7:fis isolated from wheat etiolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polynucleotide encoding delta-6 desaturase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cahoon EB, Cahoon RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Triticum aestivum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wheat; sphingolipid desaturase; membrane-bound desaturase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wheat sphingolipid desaturase #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY71555;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Page 49-50; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DUPO ) DU PONT DE NEMOURS & CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transgenic plant;
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                                                                                                                                                                                                                         Local Similarity
nes 8; Conserv
                                                                                                                                     15
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                                                                                                                                                                                                 1 WWKDKHNTHH 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-412336/35.
                                                                                                                                                                           wwkfnhnthh 220
                                                                                                                                                                                                                                                                                       469 AA;
                                                                                                                                                                                                                          Conservative
                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fatty acid
          delta-6 fatty acid desaturase; tariric acid;
                                                                                                                                                                                                                                      80.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hitz WD,
                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                    Score 59;
Pred. No.
                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kinney AJ;
                                                                                                                                                                                                                                      0.15;
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                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                Length 469;
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Search completed: August Job time: 250 sec
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                                                                                                                                             Query match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                        The present sequence is a delta-6 fatty acid desaturase protein sequence from clone pps.pk0011.d5:fis isolated from Florida bitterbush developing seed cDNA library, pps. The delta-6 desaturase enzyme catalyses the formation of tariric acid, a fatty acid that has a triple bond at the delta-6 carbon. The present sequence is useful for producing transgenic plants having altered levels of delta-6 desaturase which in turn would alter the fatty acid composition. The enzyme is also useful for producing polyclonal or monoclonal antibodies. The polynucleotide is useful as primer or probe for screening cDNA libraries to
                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Page 40-41; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polynucleotide encoding delta-6 desaturase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-412336/35.
N-PSDB; AAD01349.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                              isolate desired full-length cDNA clones.
                                                                              190 wwkldhnthh
                                                                                                                                             Local Similarity
nes 8; Conserv
                                                                                                              1 WWKDKHNTHH 10
                                                                                                                                                                                                                               448 AA;
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                                                                                                                                                           78.1%;
80.0%;
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               2001, 20:24:16
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                                                                                                                                                           Score 57; L
Pred. No. 0.
                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kinney
                                                                                                                                                                               В
                                                                                                                                                             . 29;
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                                                                                                                                                                          Length 448;
                                                                                                                                               Indels
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Minimum
Maximum
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
DB
                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq
  protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length: 0
length: 2000000000
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Match Length
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 PIR_68:*
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Listing first 45 summaries
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Gapop 10.0 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version Copyright (c) 1993 - 2000
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pir3:*
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53.4	53.4	53.4	54.1	54.1	54.1	54.8	54.8	54.8	54.8	54.8	54.8	54.8	54.8	54.8	56.2	
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S13338	T41827	H72860	Q3ECTH	140839	A35125	A46719	D86311	A86258	D84428	T14614	C84176	S37815	S67191	C70890	T12203	
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ALIGNMENTS

submitted to the EMBL Data Library, March 1996 A; Reference number: 220188 A; Accession: T26280

GB/EMBL/DDBJ

A; Experimental source: clone W08D2

A;Cross-references: EMBL:Z70271; PIDN:CAA94233.1; GSPDB:GN00022;

CESP:W08D2.4

A;Status: translated from A;Molecule type: DNA A;Residues: 1-473 <WIL>

C; Accession: T26280; T37238 R; Swinburne, J.; Ainscough, R. linoleoyl-CoA desaturase (EC 1.14.99. N;Alternate names: Delta6 fatty acid C;Species: Caenorhabditis elegans

C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000

.25) W08D2.4 - desaturase

Caenorhabditis elegans

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protein
C;Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 31-Mar-2001 C;Accession: JC7556
R;Laoteng, K.; Mannontarat, R.; Tanticharoen, M.; Cheevadhanarak, S.
Biochem. Biophys. Res. Commun. 279, 17-22, 2000
A;Title: Delta6-desaturase of Mucor rouxii with high similarity to plant delta6-desat
                                                                                                                                                                                           RESULT
JC7556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map Position: 4
A; Map Position: 4
A; Introns: 13/3; 39/2; 234/3; 277/3; 378/1; 413/3
C; Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
C; Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
C: Kerwords: alternative splicing; oxidoreductase; unsaturated fatty
                                                                                                                     linoleoyl-CoA desaturase (EC 1.14.99.25) - N;Alternate names: delta6-desaturase C;Species: Mucor rouxii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-38,69-430,'V',432-473 <NAP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Napier, J.A.; Hey, S.J.; Lacey, D.J.; Shewry, P.R. Biochem. J. 330, 611-614, 1998
A;Title: Identification of a caenorhabditis elegans
                                                                                                                                                                                                                                                                                             В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:AF031477; NID:g3088519; PIDN:AAC15586.1; PID:g3088520
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Best Local
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Pred. No.
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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, D. Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
A84900
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                                                                                                 C;Genetics:
A;Gene: At2g46210
A;Map position: 2
                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-449 <STO>
                                                                                                                                                                                                                                A; Reference number: A84420; A; Accession: A84900
                                                                                                                                                                                                                                                                                                                                                               hypothetical protein At2g46210 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: A84900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AL078610; PIDN:CAB44385.1; A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-345 <OLI>
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A; Accession: T36617
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submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable Delta6 fatty acid desaturase (EC 1.14.99.-) SCH35.42c [similarity] C;Species: Streptomyces coelicolor C;Dete: 03-Dec:1999 #sequence_revision 03-Dec:1999 #text_change 20-Jun-2000 C;Accession: T36617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-523 <LAO>
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70.0%;
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       Score 52; DB Pred. No. 0.61 0; Mismatches
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Pred. No.
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June 1999
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0.013;
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0.61;
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           Indels
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                        Query Match
Best Local
           Matches
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R;Sperling, P.; Zaehringer, U.; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A;Title: A sphingolipid desaturase from higher plants. Identification
A;Reference number: Z22986; MUID:99003197
A;Accession: T55555
                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Brassica napus (rape)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 15-Sep-2000
C;Accession: T50555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Experimental source: cultivar Columbia; BAC clone F2A19
R; Sperling, P.; Zaehringer, U.; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 198596.
A; Title: A sphingolipid desaturase from higher plants. Identification of a new A; Reference number: Z22986; MUID:99003197
A; Accession: T51848
                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-449 <SPE>
A; Cross-references: EMBL: AJ224160; PIDN: CAA11857.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; submitted to the Protein Sequence Database, January 2000 A;Reference number: 224480 A;Accession: T47950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 delta-8 sphingolipid desaturase (EC 1.14.99.-) [validated] - Arabidopsis thaliana N;Alternate names: protein F2A19.180 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000 C;Accession: T47950; T51848
                                                                                                                      C;Genetics:
A;Gene: sld1
                                                                                                                                                                      A; Experimental source:
                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     delta-8 sphingolipid desaturase [imported] -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Description: (EC 1.14.99.-); delta-8 sphingolipid desaturase [validated; C;Keywords: oxidoreductase; unsaturated fatty acid biosynthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: cultivar Columbia; mainly green parts,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-449 <SPE>
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70.0%;
                      71.28;
Score 52; DB
Pred. No. 0.61
0; Mismatches
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                      DB 2;
0.61;
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Similarity 7; Conser

Conservative

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Gaps

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R;Sperling, P.; Schmidt, H.; Heinz, E.
Eur. J. Blochem. 232, 798-805, 1995
A;Title: A cytochrome-b(5)-containing fusion protein similar
A;Reference number: S68358; MUID:96028121
A;Accession: S68358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-458 <SPE>
A;Cross-references: EMBL:X8714; NID:g1040728; PIDN:CAA60621.1;
A;Cross-references: EMBL:X8714; NID:g1040728; PIDN:CAA60621.1;
C;Superfamily: cytochrome b5 core homology
C;Keywords: heme; iron; metalloprotein; oxidoreductase
F;16-90/Domain: cytochrome b5 core homology <CB5>
F;51,74/Binding.site: heme iron (His) (axial ligands) #status pr
                                                                                                                                                                                                                                                                                                                                                                                                      R;Swinburne, J.
submitted to the EMBL Data Library,
submitted to the EMBL Data Library,
A;Reference number: Z19947
A;Accession: T24875
A;Accession: T24875
                                                                                                                                                                                                                                                                                              A;Residues: 1-197,'VSHIFNN',198-447 <WIL>A;Cross-references: EMBL:Z81122; PIDN:CAB
A;Experimental source: clone T13F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Functional identification of a fatty acid delta5 desaturase A;Reference number: 222422; MUID:99059458
A;Accession: T43319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000 C;Accession: T43319; T24875
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""" (Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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    20
                                                                                                                                                                                                         A; Map position: 4
A; Introns: 43/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-447 <MIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Michaelson, L.V.; Napier, J.A.; Lewis, M.; Griffiths, G.; Lazarus, C.M.; Stobart, FEBS Lett. 439, 215-218, 1998
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                                                                                                                                                                                                                                                     A; Gene: CESP:T13F2.1; des-5
                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                            A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AF078796; NID:g4003522; PIDN:AAC95143.1; PID:g4003523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
                                            Query Match
Best Local S
Matches 6
                                                                                                                                                            ;Introns: 43/3; 80/3; 197/3; 295/3; 318/2; 349/1;
;Superfamily: Caenorhabditis elegans Delta6 fatty;
;Keywords: oxidoreductase; unsaturated fatty acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fatty acid desaturase (EC 1.14.99.-) T13F2.1 [validated] - Caenorhabditis
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                                               Similarity 6; Conserv
                                                 Conservative
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70.0%;
                                                                  67.18;
66.78;
                                            Score 49; DB:
Pred. No. 1.8;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               October 1996
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                                                                                                                                                            acid desatur
biosynthesis
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Query Match
Best Local Similarity
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folate-binding protein precursor, placental - human (Species: Homo sapiens (man) (C;Species: Homo sapiens (man) (C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 13-Aug-1999 (C;Accession: A53315; A33417; A60442 R;Sadasivan, E.; Cedeno, M.M.; Rothenberg, S.P. J. Biol. Chem. 269, 4725-4735, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein T10P11.2.2 - Arabidopsis thallana
C;Species: Arabidopsis thallana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 24-Mar-1999
                                                                                                          A;Cross-references: GB:J02876; NID:g182413; PIDN:AAA35821.1; FR;Fretsheim, J.H.; Price, E.M.; Ratnam, M. Adv. Enzyme Regul. 29, 13-26, 1989
A;Title: Folate coenzyme and antifolate transport proteins in A;Reference number: A60442; MUID:90224692
A;Accession: A60442
C;Superfamily: נסומנפ־טוועווץ אי
F;1-21/Domain: signal sequence
                          A; Molecule type: protein
A; Residues: 68-87; 'V', 104-110, 'VR', 113-114, 'D', 116, 'X', 118-121; 174-184 <FRE>
C; Superfamily: folate-binding protein
                                                                                                                                                                                                                                                                                                                  A;Title: Homologous membrane folate binding A;Reference number: A33417; MUID:90105335 A;Accession: A33417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Characterization of the gene encoding otif for the ets encoded GA-binding protein. A;Reference number: A53315; MUID:94148914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 4
A; Introns: 35/1; A; Note: T10P11.2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Kaplan, N.; Johnson, D. hi, M.; Martienssen, R.;
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A; Residues: 1-255 < RAT>
                                                                                                                                                                                                                                                                                                                                                                                             R;Ratnam, M.; Marquardt, H.; Duhi
Biochemistry 28, 8249-8254, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-255 <SAD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A; Accession: A53315
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A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-1111 <KAP>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.38;
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        #status predicted
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58.9%;

Score Pred.

43; DB No. 9.3;

2;

Length 255

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omega 6 desaturase (EC 1.14.99.-) precursor, chloroplast - Chlamydomonas reinhardtii C;Species: Chlamydomonas reinhardtii C;Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 20-Jun-2000 C;Accession: JC5891 R;Sato, N.; Fujiwara, S.; Kawaguchi, A.; Tsuzuki, M. J. Biochem. 122, 1224-1232, 1997
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                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:D89110; NID:g1749427; PIDN:BAA13773.1; PID:g1749428
A;Experimental source: strain PR745
C;Superfamily: human 6-phosphofructokinase; 6-phosphofructokinase 1 homology
C;Keywords: ATP; glycolysis; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H. DNA Res. 4, 363-369, 1997
A;Title: Identification of open reading frames in Schizosacc A;Reference number: Z17323; MUID:98162722
A;Accession: T42087
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A; Residues: 1-350 <SAK>
A; Cross-references: GB:D14581; NID:g493223; PIDN:BAA03435.1; PID:g493225
C; Superfamily: omega-3 fatty acid desaturase
C; Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphatidylcholine desaturase (EC 1.3.1.35) - Anabaena variabilis N;Alternate names: Delta-12 desaturase; fatty acid desaturase (EC 1.14.99.-C;Species: Anabaena variabilis C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
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A; Residues: 1-359 < YOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable 6-phosphofructokinase (EC 2.7.1.11) - fission yeast (Schizosaccharomyces
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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A;Title: Identification of conserved domains
A;Reference number: S43770; MUID:94207189
A;Accession: S43772
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5; Conser
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66.7%;
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71.4%;
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Pred. No. 13;
1; Mismatches
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        Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] -C;Species: Rattus norvegicus (Norway rat) C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_C;Accession: JG0180
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C;Species: Homo sapiens (man)
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jun-2000
C;Accession: T1315; T08765
R;Cho, H.P.; Nakamura, M.T.; Clarke, S.D.
J. Biol. Chem. 274, 471-477, 1999
J. Biol. Chem. 274, 471-477, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AF126799; NID:g4406527; PID:g4406528; PIDN:AAD20018.1 R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, March 1999 A;Reference number: Z16471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: omega-3 fatty acid desaturase
C;Keywords: chloroplast; oxidoreductase
F;l-40/Domain: transit peptide (chloroplast) #status predicted
                                                                                                                                                                                                C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase; unsaturated F;18-94/Domain: cytochrome b5 core homology <CB5> F;53,76/Binding site: heme iron (His) (axial ligands) #status predicted
                                                                                                                                                                                                                                                                  C; Superfamily: cytochrome b5 core homology
                                                                                                                                                                                                                                                                                                              A; Cross-references: GDB:9956652
                                                                                                                                                                                                                                                                                                                                       A; Gene: GDB: FADSD6
                                                                                                                                                                                                                                                                                                                                                       C; Genetics
                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: adult uterus; clone DKFZp586C201
                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL: AL050118
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 'RTRG',138-428,'D',430,'M',432-444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A; Accession: T08765
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A; Residues: 1-444 < CHO>
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A; Title: Cloning,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linoleoyl-CoA desaturase (EC 1.14.99.25) [validated] - human N;Alternate names: Delta6 fatty acid desaturase; protein DKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: des6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: DDBJ:AB007640; NID:92696716; PIDN:BAA23881.1; C;Comment: This enzyme catalyzes the desaturation of monoenoic to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-424 <SAT>
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                                                                                         Matches
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                                                                                      Mismatches
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23-Jul-1999 #text_change

21-Jul-2000

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R:Aki, T.; Shimada, Y.; Inagaki, K.; Higashimoto, H.; Kawamoto, S.; Shigeta, S.; Ono, K.
Biochem. Biophys. Res. Commun. 255, 575-579, 1999
A;Title: Molecular cloning and functional characterization of rat delta-6 fatty acid des A;Reference number: JG0180; MUID:99160394
A;Rocession: JG0180
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-444 <AKID
A;Cross-references: DDBJ:AB021980; NID:94514721; PIDN:BAA75496.1; PID:94514722
C;Repords: 1-494 <AKID
A;Residues: 1-494 <AKID
A;Cross-references: DDBJ:AB021980; NID:94514721; PIDN:BAA75496.1; PID:94514722
C;Repords: heme; 1ron; metalloprotein; oxidoreductase; unsaturated fatty acid biosynthe F;18-94/Domain: cytochrome b5 core homology
C;Repords: heme; 1ron; metalloprotein; oxidoreductase; unsaturated fatty acid biosynthe F;18-94/Domain: cytochrome b5 core homology <CB5>
F;53,76/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match
Best Local Similarity 50.0%; Pred. No. 17;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WWKDKHNTHH 10
Db 212 WWNHRHFOHH 221

Search completed: August 9, 2001, 20:26:07

Job time: 246 sec
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GenCore version 4.5

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OM protein - protein search, using sw model

Run on: August 9, 2001, 20:36:50; Search time 28.86 Seconds (without alignments)
11.870 Million cell updates/sec

Title: US-09-367-013B-2_COPY_204_213

Sequence: 73

Sequence: 1 WWKDKHNTHH 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database :

SwissProt_39:*

SUMMARIES

33 33 33	, i	ız⊆
		Score
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	7.8	Query Match I
4451 451 4701 1124 4701 1124 1124 1126 1	55	Length DB
PSS_ECOLIA AURI_YEAST AURI_CORPS PLD_CORPS PLD_CORUL YIBD_ECOLIA PP15_NPVBM FD31_BTANA FD3E_FDAAG FD3E_BTANA FD3E_BTANA FD3C_BTANA FD3C_ARATH FD3C_BTANA F	FOL2_	3 ID
P23830 P238107 P238107 P203332 P206332 P211290 P4114790 P4186231 P486231 P486231 P486231 P48623 P48623 P48623 P48623 P48623 P48623 P48627 P48627 P48627 P48629 P48627 P48629	1420	Description
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RESULT 2
ACOL_YEAST
ID ACOL_YEAST
AC P21147;
DT 01-MAY-1991
DT 01-CCT-1900
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RC STRAIN-S288;
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RX MEDLINE-973
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SEQUENCE FROM N.A.
MEDLINE-91056050; PubMed-1978720;
MEDLINE-91056050; PubMed-1978720;
Stukey J.E., McDonough V.M., Martin C.E.;
"The OLE1 gene of Saccharomyces cerevisiae encodes the delta 9 fatty
"The OLE1 gene of Saccharomyces cerevisiae encodes the rat stearoyl-
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1991 (Rel. 18, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2090 (Rel. 40, Last annotation update)
ACYL-COA DESATURASE 1 (EC 1.14.99.5) (STEAROYL-COA DESATURASE 1)
(FATTY ACID DESATURASE 1).
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Yeast 13:861-869(1997).
-!- FUNCTION: UTILIZES O(2) AND ELECTRONS
B(5) DOMAIN TO CATALYZE THE INSERTION
SPECTRUM OF FATTY ACYL-COA SUBSTRATES
                                                                                 Feuermann M., de Montigny J., Potier S., Souciet J.-L.;
"The characterization of two new clusters of duplicated genes
suggests a 'Lego' organization of the yeast Saccharomyces cerevisiae
                                                                                                                                          STRAIN=S288C;
MEDLINE=97377993;
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; F
Saccharomycetales;
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EMBL; J02876; AAA35831.1; -.
EMBL; U02714; AAA17370.1; -.
EMBL; U02716; AAA17370.1; J0INED
PIR; A33417; A33417.
                                                                      chromosomes."
                                                                                                                                                                            SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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ong as its content is in
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RESULT 3
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AC P23830; P78100;
AC P23830; P78100;
DT 01-NOV-1991 (Rel. 2
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CDP-DIACYLGLYCEROL--SERINE O-PHOSPHATIDYLTRANSFERASE (EC 2.7.8.8)
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DOMAIN
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PROSITE: PS00191; CYTOCHROME_B5_2; 1.
PROSITE: PS00476; FATTY_ACID_DESATUR_1; 1.
PROSITE: PS00476; FATTY_ACID_besatur_1; 1.
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Pfam; PF00173; heme_1; 1.
PRINTS; PR00075; FACDDSATRASE.
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        SEQUENCE FROM N.A., AND SEQUENCE MEDLINE-91161632; PubMed-2002065 Dechavigny A., Heacock P.N., Dow
                                                                            Bacteria; Proteobacteria; Escherichia.
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                                                                                                   Escherichia coli
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                                                           NCBI_TaxID=562;
                                                                                                                              (PHOSPHATIDYLSERINE SYNTHASE).
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC RETICULUM (PROBABLE).

DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE AND/OR BE INVOLVED IN METAL ION BINDING.

SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.

SIMILARITY: CONTAINS A CYTOCHROME B5 FAMILY, HEME-BINDING DOMAIN.
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Endoplasmic reticulum; Heme.
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EME LIGAND (BY SIMILARITY).

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A6CC78DD4210ECCA CRC64;
                                                                                        subdivision; Enterobacteriaceae
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                            AUR1_YEAST STANDARD;
P36107; Q92324;
01-JUN-1994 (Rel. 29, Creat
01-JUN-1994 (Rel. 29, Last;
15-JUL-1998 (Rel. 36, Last;
AUREOBASIDIN A RESISTANCE P.
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                     AUR1
                                                                                                                                                                                                                                                                                                                            Transferase;
                                                                                                                                                                                                                                                                                                                                               PIR; JH0368; JH0368.
EcoGene; EG10781; ps.
InterPro; IPR001736;
                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. entities requires a license agreement (See
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-!- SUBCELLULAR LOCATION: CYTOPLASMIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meth. Enzymol. 209:287-2
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          Saccharomyces cerevisiae (Baker's
                                                                                           YEAST
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SIMILARITY: BELONGS
CLASS-II FAMILY.
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                                                                                                                                          WKDKHNTHH 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
                     OR YKLOO4W
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AE000345; AAC75638.1;
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Fungi;
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Ascomycota;
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R -> DD (IN REF. 1).
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LL -> FV (IN REF. 1).
P -> S (IN REF. 1).
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Pred. No.
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Saccharomycotina;
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Saccharomycetes;
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EMBL; Z28004; CAA81836.1; -.
PIR; S37815; S37815.
SGD; S0001487; AUR1.
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Thierry A.
                   Kondo A., Hashida-Okado T., Takesako K., Kato I.; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases
                                         SEQUENCE FROM N.A
STRAIN-TIMM 0136;
                                                                        Eukaryota; Fungi;
Saccharomycetales;
NCBI_TaxID=5476;
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Saccharomyces cerevisiae: a
Aur1p-depleted cells.";
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Hashida-Okado T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 er J., Pascolo S., Richard G.F., Ghazvini Merry A., Monnier A.L., Dujon B.; all printed (MAR-1994) to the EMBL/GenBank/DDBJ FUNCTION: ESSENTIAL FOR GROWTH, WILD TYPE FOR AUREOBASIDIN A (ABA). MAY HAVE A ROLE FOR MUREOBASIDIN A (ABA).
         SUBCELLULAR LOCATION:
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                                                                                                                                                                                                                                                                                     Similarity 50.
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                                                                                   Ascomycota; mitosporic
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Ogawa A., Endo
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          INTEGRAL MEMBRANE
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AUR1 FAMILY
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P20626; Q59314;
01-FEB-1991 (Rel
                                                                                                              SEQUENCE FROM N.A.
STRAIN-BIOVAR EQUI / ISOLATE 155;
STRAIN-BIOVAR EQUI / ISOLATE 155;
MEDLINE-95255653; PubMed-7737503;
MCNamara P.J., Cuevas W.A., Songer J.G.;
MCNamara P.J., Cuevas D. of Corynebacterium
"Toxic phospholipases D of Corynebacterium haemolyticum:
 McNamara F
"Targeted
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-BIOVAR OVIS MEDLINE-90093451; P
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NCBI_TaxID=1719;
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                                                                                                                                                                                                                                                                                                                                                        phospholipase D gene from Cor
Bacteriol. 172:1256-1261(1990)
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              P.J., Bradley
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 mutagenesis
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58:131-136(1990).
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                              S / ISOLATE WHETTEN PubMed=7934899;
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y G.A.,
of the
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pseudotuberculosis.";
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                                                                 homology.";
Gene 156:113-118(1995).
-!- FUNCTION: HAS SPHINGOMYELINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE VARIANT
                                                                                             MCNamara P.J., Cuevas W.A., Songer J.G.;
"Toxic phospholipases D of Corynebacterium ulcerans and Arcanobacterium haemolyticum: homology.";
                                                                                                                                 MEDLINE=95255653; PubMed=7737503;
                                                                                                                                                                                                                                PLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       decreased virulence of Corynebacterium pseudotuberculosis.";
mol. Microbiol. 12:921-930(1994).
-:- FUNCTION: VIRULENCE FACTOR AFFECTING BACTERIAL DISSEMINA
SURVIVAL WITHIN THE HOST. HAS MAGNESIUM-DEPENDENT SPHING
AND HEMOLYTIC ACTIVITY.
-:- CATALYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H(2)0 - CHOL
        This
                                                                                                                                              SEQUENCE FROM N.A. STRAIN=ATCC 739;
                                                                                                                                                                                        Corynebacterium
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SIMILARITY: TO
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        SWISS-PROT entry is copyright.
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SEQUENCE
                                    EMBL; X06690; CAA29885.1; -.
PIR; A30268; Q3ECTH.
PIR; B33276; B33276; B33276.
ECOGENE; EG11266; YibD.
InterPro; IPR001173; -.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase.
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J. Biol. Chem. 264:5226-5232(1989).
-!- SIMILARITY: BELONGS TO THE GLYC
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STRAIR-K12 / MG1655;
MEDLINE-94316500; PubMed-8041620;
Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
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Aronson B.D., Somerville R.L., Epperly B.R., Dekker E.,
"The primary structure of Escherichia coli L-threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Analysis of the Escherichia coli genome. region from 76.0 to 81.5 minutes."; Nucleic Acids Res. 22:2576-2586(1994).
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                                          Bombyx mori nuclear polyhedrosis viru
Viruses; dsDNA viruses, no RNA stage;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                        EMBL; L22858; AAA66717.1; Coat protein.
                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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          SEQUENCE FROM N.A
                               NCBI_TaxID=10458;
                                                                                                    01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-94303173; pubMed=8030224;
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R
"The complete DNA sequence of Autographa californica nuclear
polyhedrosis virus.";
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MEDLINE-97186699; PubMed-9034315;
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(Rel. 32, Last sequence up)
(Rel. 35, Last annotation KDA CAPSID PROTEIN.
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01-NOV-1991 (Rel. 2
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"Characterization of a domain of the genome of Efunctional gene for a small capsid protein and I functional gene for a small capsid protein and I functional gene for a small capsid protein and I functional gene for a small capsid protein and I functional general gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                          Transposable element. SEQUENCE 256 AA; 28409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X56644; CAA39965.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rodicio M.R.,
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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01-NOV-1995 (Rel. 32
01-FEB-1996 (Rel. 33
0MEGA-3 FATTY ACID [
FD3E_TOBAC
P48626;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yadav N.S., Wierzbicki A., Aegerter M., Caster C.S., Perez-Grau L., Kinney A.J., Hitz W.D., Booth J.R. Jr., Schweiger B., Stecca K.L., Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H., Feldmann K.A., Pierce J., Browse J., "Cloning of higher plant omega-3 fatty acid desaturases."; Plant Physiol. 103:467-476(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oxidoreductase; Fatty acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00487; FA_desaturase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L22962; AAA61775.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant Physiol. 103:467-476(1993).
-!- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brassicales; Brassicaceae; Brassica
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                                                                                                                                                                                                          124 WRISHRTHH
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SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE S
AND/ OR BE INVOLVED IN METAL ION BINDING.
SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHOLIPIDS
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5; Conserv
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(Rel.
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32, Last sequence update)
33, Last annotation update)
D DESATURASE, ENDOPLASMIC RE
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226
251
96
132
299
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55.6%;
  Last sequence update)
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POTENTIAL.

HISTIDINE BOX 1.

HISTIDINE BOX 2.

HISTIDINE BOX 3.

HISTIDINE BOX 3.
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                                                                                                                                                                                                                                                                                                                                                           Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
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RESULT 14
FD3E_PHAAU
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Best Local
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01-OCT-1993
01-FEB-1996
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DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hamada T. "Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
NCBI_TaxID-4097;
          Phaseolus aureus (Mung bean) (Vigna radiata).
Eukaryota; Viridiplantae; Embryophyta; Trache
Magnoliophyta; eudicotyledons; core eudicots;
Fabales; Fabaceae; Papillonoideae; Vigna.
                                                                                                                                                                      FD3E
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                                                                                                OMEGA-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-95011632; PubMed-7926817;
Hamada T., Kodama H., Nishimura M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Last annotation update)
OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-).
                                                                                  (INDOLE-3-ACETIC
                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D26509; BAA05515.1; -.
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                                                                                                                                                                                                                                            129
                                                                                                                                                                                                                                                                      2 WKDKHNTHH 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE (
AND/ OR BE INVOLVED IN METAL ION BINDING.
SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCT THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHOLIPIDS
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                                                                                                                                                                     PHAAU
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reductase; Fatty acid biosynthesis;
                                                                                                                                                                                                                                                                                                Similarity
5; Conserv
                                                                                             1993 (Rel. 27, Created)
1993 (Rel. 27, Last sequence update)
1996 (Rel. 33, Last annotation update)
FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of a cDNA encoding tobacco
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236
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POTENTIAL.
HISTIDINE BOX 1.
HISTIDINE BOX 2.
HISTIDINE BOX 3.
HISTIDINE BOX 3.
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Pred. No.
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l; Mismatches
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                          core eudicots;
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omega-3
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33;
                         Tracheophyta; Spermatophyta.dicots; Rosidae; eurosids I;
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                                                                                                                                                                                                                                                                                                                             fatty acid
                                                                                                                                                                                                                                                                                                                             Length 379;
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FD3E_SOYBN
P48625;
01-FEB-1996
01-FEB-1996
01-OCT-1996
TISSUE-Seed;
MEDLINE-94302147; PubMed-8029334;
Yaddv N.S., Wierzbicki A., Aegerter M., Caster C.S., Perez-Grau L.,
Yaddv N.S., Wierzbicki A., Aegerter M., Schweiger B., Stecca K.L.,
Kinney A.J., Hitz W.D., Booth J.R. Jr., Schweiger B., Stecca K.L.,
Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H.,
Allen S.M., Blackwell M., Browse J.;
                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Last 01-CT-1996 (Rel. 34, Last 01-CT-1996 (Rel. 34, Last OMEGA-3 FATTY ACID DESATIONAL CAPTO
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between
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-i-function: MICROSOMAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRO THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO UT CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER PHOSPHOLIPIDS.
                                                                                                                                    Magnoliophyta; eudicotyledons; core eudicots; Rosidae Fabales; Fabaceae; Papilionoidaea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Hypocotyl;
Yamamoto K.T., Mori H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                Glycine max (Soybean)
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SEQUENCE FROM
                                                                                               SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
INDUCTION: BY AUXIN, ETHYLENE AND WOUNDING.
DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE S
AND/ OR BE INVOLVED IN METAL ION BINDING.
SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
                                                                                                                                                                                                                                                                                                                                                WRISHRTHH
                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 5; Conser
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208
238
97
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Search completed: August 9, 2001, 20:36:51 Job time: 700 sec
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Plant Physiol. 103:467-476(1993).
-I- FUNCTION: MICROSOMAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L22964; AAA61777.1; -.
PIR; JQ2338; JQ2338.
InterPro; IPR001225; -.
Pfam; PF00487; FA_desaturase; 1.
Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
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PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.

SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.

SUBCELLULAR LOCATIONE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE AND/ OR BE INVOLVED IN METAL ION BINDING.

SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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HISTIDINE BOX 3.
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Title:
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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O61388;
O1-AUG-1998
O1-AUG-1998
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                                     PROSITE;
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"Identification of a Caenorhabditis elegans Delta6-fatty-acid-desaturase by heterologous expression in Saccharomyces cerevisibiochem. J. 330:0-0(0).

EMBL; AF031477; AAC15586.1; -.
Interpro; IPR000566; -.
Interpro; IPR001199; -.
PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
SEQUENCE 443 AA; 51740 MW; 9513CA7C5A7E9A06 CRC64;
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"Expression of a borage desaturase cDNA containing an N-terminal cytochrome b5 domain results in the accumulation of high levels delta6-desaturated fatty acids in transgenic tobacco.";
Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
      SEQUENCE
                                                                                                                                                              investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z70271; CAA94233.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Swinburne J., Ainscough Submitted (MAR-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Rhabditidae; Pelode
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                       InterPro; IPR000566; -
InterPro; IPR001199; -
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PS50255; CYTOCHROME_B5_2; 1.
PS00213; LIPOCALIN; UNKNOWN_1
443 AA; 51772 MW; 9513D61
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Q9UVV3;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DELTA-6 FATTY ACID DESATURASE.
                MEDLINE-19400000; runned J.M., Bobik E.G. Jr., ruan L., Huang Y.S., Chaudhary S., Thurmond J.M., Bobik E.G. Jr., ruan L., Chan G.M., Kirchner S.J., Mukerji P., Knutzon D.S.; "Cloning of deltal2- and delta6-desaturases from Mortierella alpina "Cloning of delta12- and delta6-desaturases from Mortierella alpina"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mortierella fungus. Ge fungus, Aspergillus."; Gene 238:445-453(1999).
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and recombinant
cerevisiae.";
                                                                                                MEDLINE=99406036;
Huang Y.S., Chaudh
                                                                                                                                                                                                                                                                                     Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                  Mortierella alpina
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PROSITE; PS00191; CYTOCHROME_B5_1; UNKNOWN_1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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EMBL; AB020032; BAA85588.1; -.
HSSP; P04166; 1B5M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sakuradani E., Kobayashi M., Shimizu S.; "Delta 6-Fatty acid desaturase from an arachidonic acid-producing mortierella fungus. Gene cloning and its heterologous expression
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Ming-Chun L., Li L., Guo-Wu H., Li
Ming-Chun L., Li L., Guo-Wu H., Li
"Cloning and sequencing analysis of
from Mortierella isabellina.";
Junwu xitong 0:0-0(2001).

R EMBL; AF306634; AAG33104.1; -.

R EMBL; AF306634; AAG33104.1; -866
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Best Local 9
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Best Local
   SEQUENCE FROM N.A.

Xing L., Liu L., Hu G., Zhang L.;

Xing L., Li M., Liu L., Hu G., Zhang L.;

"Expression of Mortierella alpina delta 6-fatty acid design accharomyce cerevisiae.";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases

EMBL; AF307940; AAAG45092.1;

SEQUENCE 457 AA; 51885 MW; 480ACODD15D19DA1 CRC64;
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01-MAR-2001 (TrEMBLrel 16, 1
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Mortierella.
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Pfam; PF00173; heme_1; 1.
PROSITE; PS00191; CYTOCHROME_B5_1;
PROSITE; PS50255; CYTOCHROME_B5_2;
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NCBI_TaxID=64518;
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Best Local S
Matches 10
                                                                                    SEQUENCE FROM N.A.

STRAIN-HEDW. B. S. G.;

White T. Schmidt H., Zaehringer U., Reski R., H.

"Identification of a novel delta 6-acyl-group de:

"Identification in physcomitrella patens.";

Plant J. 15:39-48(1998).

Plant J. 15:39-48(1998).

-1- SIMILARITY: TO CYTOCHROME B5 DOMAIN.

EMBL; AJ222980; CAA11033.1; -.

HSSP; P04166; 1B5M.
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Q9HDG8;
01-MAR-2001 (TrEMBLr
01-MAR-2001 (TrEMBLr
01-MAR-2001 (TrEMBLr
DELTA-6 DESATURASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9ZNW2;
Q9ZNW2;
Q1-MAY-1999
Q1-MAY-1999
Q1-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence up
01-MAR-2001 (TrEMBLrel. 16, Last annotation
DELTA6-ACYL-LIPID DESATURASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun.
EMBL; AR296076; AAG36960.1; -.
EMBL; AF290983; AAG36959.1; -.
SEQUENCE 523 AA; 60622 MW;
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STRAIN-ATCC 24905;
MEDLINE-20563795; PubMed-11112411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Funariidae; Funariales; Funariaceae;
RCBI_TaxID=3218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Physcomitrella patens (Moss).
Eukaryota; Viridiplantae; Embryophyta; Bryophyta;
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   PROSITE;
                              Pfam; PF00173;
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Mucor rouxii with high similarity to
its heterologous expression in Sacci
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Pred. No.
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Q9F2M3;
01-MAR-2001 (TrEMBLrel. 16, Creat
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01-MAR-2001 (TrEMBLrel. 16, Last
PUTATIVE FATTY ACID DESATURASE.
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STRAIN-WT3; TISSUE-PROTONEMATA;
                                                                                                                                                                                                                               Q9LEM9 PRELIMINARY; PRT; Q9LEM9; 01-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control
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SEQUENCE
                                                                                                                          Ceratodon purpureus (Moss).
Eukaryota; Viridiplantae; Embryophyta;
Dicranidae; Dicranales; Ditrichaceae;
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Cerdeno A.M., Parkhill J., B
Submitted (SEP-2000) to the
                                                                                                     NCBI_TaxID=3225;
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"A set of ordered cosmids and a detailed genetic and
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Microbiol. 21:77-96(1996).
Microbiol. 21:77-96(1996);
; AL442669; CAC10296.1; -
ENCE 350 AA; 38678 MW; 240C0BA/
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8; Conservative
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(SEP-2000) to
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e EMBL/GenBank/DDBJ databases.
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Pred. No. 0.02
0; Mismatches
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Pred. No. (
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annotation update)
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                                                                                                                                    ; Bryophyta; Bryopsida;
Ceratodon.
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Q9ZTU8
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Q9ZTY9
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Best Local
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Best Local (
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Q9ZTY9;
Q1-MAY-1999
Q1-MAY-1999
Q1-MAR-2001
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SEQUENCE
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$276.
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Q9ZTU8
Q9ZTU8;
Q1-MAY-1999
Q1-MAY-1999
Q1-MAR-2001
                                                                                                                                                                                                                                                           -I- SIMILARITY: TO CYTOCHROME B5
EMBL; AF031194; AAD10250.1; -
HSSP; P04166; 1AWP.
Mendel: 35849; Triae; 2419; 35849.
InterPro; IPR001199; -
InterPro; IPR001199; -
                                                                                                                                                                              Pfam: pF00173; heme_1: 1.
PRINTS: PR00363; CYTOCHROMEB5.
PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
PROSITE: PS00038; HELIX_LOOP_HELIX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001199; -...
Pfam; PF00173; heme_1; 1.
PR051TE; PS50255; CYTOCHROME_B5_2; 1.
SEQUENCE 520 AA; 59160 MW; 5A9332EECC153439 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              moss Ceratodon purpureus. A new member of the cytochrome superfamily.";
                                                                                                                                                                                                                                                                                                                                                  Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
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Delhaize E., He
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                                                                                                                                                                                                                                             InterPro; IPR003015;
                                                                                                                                                                                                                                                                                                                                                                                 Pelhaize E., Hebb D.M.,
"Aluminum tolerance in
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211 WWKFNHNTHH
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MEDLINE-97268723; PubMed-9108131;

Sayanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,

Christie W.W., Shewry P.R., Napier J.A.;

"Expression of a borage desaturase cDNA containing an N-terminal cytochrome b5 domain results in the accumulation of high levels c delta6-desaturated fatty acids in transgenic tobacco.";

Proc. Natl. Acad. Sci. U.S.A. 94:4211-4218(1997).

-i-SIMILARITY: TO CYTOCHROME B5 DOMAIN.

EMBL; AF005096; AAD01240.1;

EMBL; AF005191; 1WDB.
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Ricinus communis (Castor bean).

Ricinus communis (Castor bean).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;

Malpighiales; Euphorbiaceae; Ricinus.
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Kinashi H., Hopwood D.A.; Rinashi H., Hopwood D.A.; ast of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
EMBL; ALO78610; CAB44385.1; -
SEQUENCE 345 AA; 38022 MW; 1C938614F662DC3A CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-A3(2);
Bentley S.D., Parkhill J., I
Submitted (JUN-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oliver K., Harris D.,

"A set of ordered cosmids and a detailed genetic and physical

"A set of ordered cosmids and a detailed genetic and physical

the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PUTATIVE_DELTA FATTY ACID DESATURASE.
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MEDLINE-97000351; PubMed-8843436;
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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PROSITE; PS50255; CYTOCHROME_B5_2;
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80.0%;
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Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;
Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
NCBI_TaxID-3225;
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Sperling P., Lee M., Girke T., Zaehringer U., Stymne S., F
"A bifunctional delta 6-fatty acyl acetylenase/desaturase
moss Ceratodon purpureus. A new member of the cytochrome b
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Pfam; PF00173; heme_1;
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EMBL; AJ250734; CAB94992.1; -.
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ALIGNMENTS

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99US-0145089. 99US-0145192. 99US-0145145. 99US-0145218. 99US-0145224.

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ID AAW8
AXX AAW8
AX AAW8
AX AAW8
AX Desa
XX Fatt
KW malh
KW canc
KW concl
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21-OCT-1999;
22-OCT-1999;
22-OCT-1999;
22-OCT-1999;
                           The present sequence represents a peptide derived from a desaturase enzyme. The specification describes methods for desaturating a fatty acid and for producing a desaturated fatty acid by expressing increased levels of a desaturase. Desaturases can be used for desaturating fatty acids. The enzymes can be used to produce polyunsaturated fatty acids, which can be used for treating malnutring polyunsaturated fatty acids, which can be used for treating malnutring the produce polyunsaturated fatty acids, which can be used for treating malnutring the produce polyunsaturated fatty acids, which can be used for treating malnutring the produce polyunsaturated fatty acids, which can be used for treating malnutring the produce polyunsaturated fatty acids, which can be used for treating malnutring the produce produce polyunsaturated fatty acids, which can be used for treating malnutring the produce pro
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                                                                                                                                                                                                                                                                                                                                                          New isolated fatty acid desaturase enzymes - use of polyunsaturated fatty acids for use in, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chaudhary S, Thurmond J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
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                                                                                                                                                                                                                                                               Example 2; Pages 101-102; 165pp;
                                                                                                                                                                                                                                                                                                                                   compositions, nutritional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-594582/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-APR-1997;
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   pharmaceutical compositions,
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                                                                                                                                                                                                                                                                                                                            acids for use in, e.g. pharmaceutical compositions, cosmetics or animal fe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypertension; inflammatory skin disorder
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      in cosmetics or in animal feed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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7-JUL-1999; 8-JUL-1999; 2-AUG-1999;

S-0145919. S-0145951. S-0146386.

S-0147038. S-0147204.

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CC desaturase enzyme. The enzyme sequence is used in the methods of the invention. The specification describes methods for desaturating a CC fatty acid and for producing a desaturated fatty acid by expressing CC increased levels of a desaturase. The present desaturase is an enzyme CC which introduces a double bond carbons 6 and 7 from the carboxyl end of CC a fatty acid molecule. The enzyme can be used for desaturated fatty acids. The enzyme can be used for treating malnutrition, in pharmaceutical CC compositions, in cosmetics or in animal feed. The polyunsaturated fatty acids can be used for treating e.g. restenosis after angioplasty, CC inflammation, rheumatoid arthritis, asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure. They can also be used to inhibit platelet aggregation, cause vasodilation, lower cholesterol level:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
AAW84137
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Best Local S
Matches 5
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26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fatty acid; delta-6 desaturase; polyunsaturated fatty acid; malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis; cancer; diabetes; eczema; platelet aggregation; vasodilation; cholesterol level; endometriosis; premenstrual syndrome; myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis; acute respiratory syndrome; hypertension; inflammatory skin disorder.
                                                                                                                                                                                                                                           New isolated fatty acid desaturase enzymes \cdot used for the production of polyunsaturated fatty acids for use in, e.g. pharmaceutical compositions, nutritional compositions, cosmetics or animal feed
                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                  WPI; 1998-594582/50
N-PSDB; AAV63624.
                                                                                                                                                                                                                                                                                                                                          Chaudhary S, Thurmond J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A delta-6 desaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW84137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mortierella alpina.
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CALGENE LLC
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                                                                                                                                                                                                                Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163
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                                                                                                                                                                                                                                                                                                                                                       Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           990S-0161359.
990S-0161360.
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990S-0161992.
990S-0161993.
990S-0162142.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                        Leonard AE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                       Mukerji P;
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18-CCT-1999
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reduce
caused
                                                                                                                                    Nucleic acid construct able to express fatty a plants - useful in human or animal nutrition, therapeutically, e.g. for restenosis, cancer a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             caused by non-steroidal anti-inflammatory drugs, prevent or treat endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis and chronic fatigue after viral infections, treat AIDS, multiple
          coupled to an expression control sequence functional in plants. Recombinant plant cells containing at least one DNA encoding a M. alpina fatty acid desaturase (FAD), can be used for the production of
                                               relates to a nucleic acid construct that contains at least one of the nucleotide sequences (AAX00889 to AAX00891) encoding M. alpina delta delta 12 and delta 5 desaturases (AAW95504 to AAW95506) respectively,
                                                                                                                Claim
                                                                                                                                                                                                                                            Chaudhary
                                                                                                                                                                                                                                                                 (ABBO
(CALJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW95504 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
 fatty acid desaturase (FAD),
polyunsaturated fatty acid (
                                                                                                                                                                                           N-PSDB; AAX00889
                                                                                                                                                                                                    WPI; 1999-080739/07.
                                                                                                                                                                                                                                                                                                                  11-APR-1997;
11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                     10-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                     WO9846764-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mortierella alpina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic; stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula; dietary supplement; prostaglandin; restenosis; angioplasty; inflammation; rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mortierella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sclerosis, acute respiratory syndrome, hypertension and inflammatory skin
                                                                                                                                                                                                                              Thurmond
                                                                                                                                                                                                                                                                                                                                            24-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inhibit proliferation of vessel wall smooth muscle and fibrous tissue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 hdflh 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 HDFLH 5
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                                                                                       represents
                                                                                                                                                                                                                                                                ) ABBOTT LAB.
) CALGENE LLC.
                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 desaturase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ьy
                                                                                                                                                                                                                       / S,
                                                                                                             Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prevent gastro-intestinal bleeding and other side effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cosmetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alpina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                               3A-E;
                                                                                                                                                                                                                                          Huang
                                                                                                                                                                                                                                                                                                    97US-0833610.
97US-0834033.
97US-0834655.
                                                                                                                                                                                                                                                                                                                                            97US-0956985
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                                                                                      Mortierella alpina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            delta 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide; 457
                                                                                                            210pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recombinant;
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                                                                                                                                                                                                                                          Knutzon
 (PUFA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            desaturase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     feed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fatty acid desaturase; FAD;
  These
                                                                                                                                                                                                                                          Leonard AE,
                                                                                      delta 6 desaturase. The
  recombinant cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                        , as
                                                                                                                                                              acid desaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                        cosmetics
diabetes
                                                                                                                                                                                                                                          Mukerji P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                      invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUFA;
 plants
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        production of PUFA (or their metabolites such as prostaglandins), e.g. restenosis after angioplasty, inflammation, AIDS, rheumatold arthritis, psoriasis, osteoporosis, cancer, eczema, diabetes; (1v) as cosmetics, and (v) as animal feeds. Fragments of the DNA are used as probes to isolate related coding sequences. Recombinant plants can produce high yields of PUFA, since new pathways can be created and unwanted ones suppressed. Plants can be engineered to express oils of particular PUFA composition, e.g. one similar to that in human milk, and product recovery is simpler
                                                                                                                                                                                                            (ABBO )
(CALJ )
                                                                                                                                                                                                                                                                                                                                                                                   cancer; diabetes; eczema; platelet aggregation; vasodilation;
cholesterol level; endometriosis; premenstrual syndrome;
myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
acute respiratory syndrome; hypertension; inflammatory skin disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A delta-6 desaturase enzyme amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dietary supplements or substitutes, for use in humans or animals; for treating disorders associated with inadequate consumption or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arachidonic acid, gamma-linolenic acid, stearidonic acid and elcosapentaenoic ac
                                                                                                    New nucleic acid encoding delta5 and other desaturase enzymes useful in production of oils of increased arachidonic acid con
                                                                                                                                                                                    Chaudhary
                                                                                                                                                                                                                                                                                                                                  W09846765-A1
                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                          malnutrition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW85121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW85121 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stearidonic acid and eicosapentaenoic acid (EPA). These plant oils used: (i) to treat malnutrition; (ii) in infant feeding formulas,
                                                                                                                                            WPI; 1999-009334/01
                                                                                                                                                                     Thurmond
                                                                                                                                                                                                                                                                              10-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     containing them are used to produce oils such as linoleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 hdflh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 HDFLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with
                                                                                                                                                                                                                                                                                                                                                                                                                                         acid; delta-6 desaturase; polyunsaturated fatty aci
trition; inflammation; rheumatoid arthritis; asthma;
                                                                                                                                                                                                             ABBOTT LAB.
CALGENE LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
5; Conserv
                                                                                                                                                                  J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e.g. fish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   457
                                                              Pages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                 Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                     97US-0833610
                                                                                                                                                                                                                                                                              98WO-US07422
                                                              95-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                    Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                        cancer,
                                                                                                                                                                                    Knutzon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
Pred.
                                                                                                                                                                                    Ò
                                                              English
                                                                                        as foods,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
                                                                                                                                                                                    Leonard AE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dihomo-gamma-linolenic
                                                                                          animal feeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid;
                                                                                                                                                                                    ٦,
                                                                                                                                                                                                                                                                                                                                                                                                                                          psoriasis;
                                                                                          cosmetics
                                                                                                        content,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oils
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (111)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           are
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The present sequence represents a fatty acid delta-6 desaturase enzyme. The specification describes methods for desaturating a fatty acid and for producing a desaturated fatty acid by expressing increased levels o a desaturase. The present desaturase is an enzyme which introduces a

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RESULT
AAY92599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double bond carbons 6 and 7 from the carboxyl end of a fatty acid molecule. The enzyme can be used for desaturating fatty acids. The enzyme can be used to produce polyunsaturated fatty acids, which can be used for treating malnutrition, in pharmaceutical compositions, in cosmetics or in animal feed. The polyunsaturated fatty acids can be used for treating e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis, asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure. They can also be used to inhibit platelet aggregation, cause vasodilation, lower cholesterol levels, inhibit proliferation of vessel wall smooth muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding and other side effects caused by non-steroidal anti-inflammatory drugs, prevent or treat endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis and chronic fatigue after viral infections, treat myalgic encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                   transgenic insect cell; polyunsaturated long chain tatty acid; antilnflammatory; antirheumatic; antiasthmatic; antipsoriatic; osteopathic; cytostatic; antidiabetic; dermatological; gynecological; anti-HIV; neuroprotective; hypotensive; nephrotropic; vasodilator;
                                                                                                                                                                                                                                                                                                                                                             Key Location/Qualifiers Misc-difference 172..176
   N-PSDB; AAA09430
                                                Mukerji P, Huang Y,
                                                                               (ABBO ) ABBOTT
                                                                                                              05-OCT-1998;
                                                                                                                                              29-SEP-1999;
                                                                                                                                                                           13-APR-2000
                                                                                                                                                                                                          W0200020602-A2
                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                             Mortierella alpina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      delta-6 desaturase; gamma-linolenic acid; biosynthesis;
transgenic insect cell; polyunsaturated long chain fatty acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M. alpina delta-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY92599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY92599 standard; Protein; 457 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sclerosis, acute respiratory syndrome, hypertension and inflammatory skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 hdflh 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 HDFLH 5
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                     2000-328935/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                LAB.
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                                                                                                                                            99WO-US22686
                                                                                                                                                                                                                                                                                                                                                                                                                                           vasotropic.
                                                                                                                                                                                                                                                                                                                /label histidine_box
/note "conserved among
209..213
                                                                                                                                                                                                                                                                       /note= "conserved among membrane-bound
395..399
                                                                                                                                                                                                                                                         /label=
                                                                                                                                                                                                                                                                                                   /label= histidine_box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fatty acid desaturase
                                                  Parker-barnes JM,
                                                                                                                                                                                                                                     "conserved among membrane-bound
                                                                                                                                                                                                                                                         histidine_box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                 membrane-bound desaturases"
                                                  Das
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                  7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 457;
                                                                                                                                                                                                                                        desaturases'
                                                                                                                                                                                                                                                                                    desaturases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT
AAY56045
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Best Local Similarity
Thes 5; Conserve
X PXX PTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            residues 50-53, 39-43, 172-176, 204-213, or 390-402 of delta-5 desaturase (AAY9560) or comprising delta-12 desaturase (AAY9560) are claimed. Oil and fatty acids (especially gamma-linolenic acid) isolated from the recombinant insect cells are also claimed. Production of polyunsaturated long chain fatty acids (PUFAs) in insect cells has many advantages, as insect cells have greatly simplified lipid compositions, are not subject to external variable fluctuations, and can easily be maintained and manipulated. The oils are used in pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              compositions, infant formulas, dietary supplements or substitutes, and cosmetics (all claimed). The PUFA supplements have antiinflammatory, antirheumatic, antiasthmatic, antipsoriattic, osteopathic, cytostatic, antidiabetic, dermatological, gynecological, anti-HIV, neuroprotective,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid to linoleic acid, linoleic acid to gamma-linolenic acid or of alpha-linolenic acid to stearidonic acid. Transgenic insect cells comprising a nucleotide sequence which encodes a polypeptide compr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel transgenic insect cells comprising a nucleotide sequences which encode delta-6-desaturase or delta-12- desaturase, useful for productionly-unsaturated long chain fatty acids, e.g. arachidonic acid
             Disclosure; Fig 9; 71pp; English
                                              Producing essential fatty acids and long-chain acids, for use in nutritional, animal feed and
                                                                                              WPI; 2000-072619/06.
N-PSDB; AAZ47129.
                                                                                                                                                                                                                                                                                                                                                 Unidentified.
                                                                                                                                                                                                                                                                                                                                                                              Polyunsaturated fatty acid; fungus; delta6-desaturase; animal transgenic animal; malnutrition; biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                              Fungal delta6-desaturase protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY56045 standard; Protein; 457 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The fatty acid desaturases are able to catalyse the conversion of oleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 145-146; 170pp; English.
                                                                                                                                              Kopchick JJ,
                                                                                                                                                                            (OHIS ) UNIV
                                                                                                                                                                                                                                               28-MAY-1999;
                                                                                                                                                                                                                                                                               02-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypotensive, nephrotropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 hdflh 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 HDFLH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 457 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                               OHIO STATE
                                                                                                                                              Kelder B,
                                                                                                                                                                                                                98US-0087578
                                                                                                                                                                                                                                                99WO-US12088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 32; DB 100.0%; Pred. No. 52;
                                                                                                                                             Huang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vasodilator, antiaggregant and vasotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                              Kirchner SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                              medical formulations
                                                                                                                                              Mukerji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence corresponds to a fungal delta6-desaturase whose coding sequence is an example of a nucleic acid sequence used to transform the cells. The essential FAs obtained can be used in nutritional formulations or animal feed formulations. The long chain PFAs can be used in nutritional feed formulations. The products can also be used for productly transgenic animals which can be used for producing transgenic animals which can be used for producing essential FAs which can be used for products such as leukotrienes, thromboxanes, arachidonic acid, elcosapentaenoic acid or docosahexaenoic acid. The products can also be used in cell culture. The animal or milk fat produced can be administered
                                                                                                                                                                                                                                                                                      New compositions comprising cells that express desaturases and elongases, for synthesizing essential fatty acids or long-chain polyunsaturated fatty acids, used in nutritional, cosmetic or are feed formulations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    delta6 desaturase; desaturase gene; elongase gene; fatty acid; elcosanold; nutrition; infant formula; dietary supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB31684 standard; Protein; 457 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method of generating novel compositions comprising animal cells producing essential fatty acids (FAs). The animal cells are produced by transforming cells, e.g. embryonic stem cells, with nucleic acid encoding heterologous enzymes involved in fatty acid, e.g. long chain or polyunsaturated fatty acid (PFA) biosynthesis. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JUL-2000; 2000WO-US19011.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mortierella alpina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-APR-2001
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produce animal cells expressing a desaturase gene and/or an elongase gene. Compositions comprising cells of the invention are useful for synthesising essential fatty acids, their derivatives or downstream products, as well as altered levels of long-chain polyunsaturated
                                                                                                                                                             The present sequence represents a delta6 desaturase.
                                                                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kopchick JJ, Kelder B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYOH-) UNIV OHIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid
                                                                                                                            polynucleotide sequence was used to trasfect mammalian cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 hdflh 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-182622/18
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF25234.
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                                                                                                                                                                                                                         Fig 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0351525
                                                                                                                                                                                                                   93pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              animal feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of a fungal delta6 desaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
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                                                                                                                                                             The desaturase
                                                                                                                                                                                                                                                                                                                   or animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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Best Local Similarity
Thes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
by (I); (b) an expression cassette (EC) containing (I) linked to one or more regulatory sequences; (c) a vector containing (I) and EC; (d) organisms containing (I), EC or the vectors of (c); (e) preparation of unsaturated fatty acids (A) or triglycerides (TG) with increased content of (A) by introducing (I) or EC into an oil-producing organism; (f) proteins (IIa) of 172 aa or 178 aa (given in the specification); (g) production of (A) or TG by using (Ia); and (h) (A) and TG produced by method (g). (I) are used to produce transgenic plants (or other organisms) that produce oils or triglycerides (TG) with increased content of unsaturated fatty acids (A) and to isolate related sequences by nutrition (e.g. Infant foods), animal feeds, pharmaceuticals and cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can be used to suppress expression of (II), resulting in oils with
                                                                                                                                                                                                                     This invention describes a novel isolated nucleic acid (I) encoding polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase activity. The invention also describes (a) amino acid sequences encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transgenic cosmetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          formulae, e.g. infant formula, dietary supplements or dietary substitutes for both humans and animals. The compositions are also useful in cosmetic or animal feed formulations. Furthermore, the compositions may also be used as fat free media or as research reagents.
                                                                                                                                                                                                                                                                                                                                  Nucleic acid encoding delta6-acetylenase producing plant oils with increased conte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1999;
22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ceratodon purpureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C. purpureus delta6-acetylenase/delta6-desaturase SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB46435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                Heinz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-2000; 2000WO-EP05274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 - DEC - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB46435 standard;
                                                                                                                                                                                                                                                                                    Example 8; Page 44-46; 69pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BADI ) BASF AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200075341-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fatty acids and eicosanoids. The compositions are useful in nutritional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 hdflh 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 HDFLH
                                                                                                                                                                                                                                                                                                                                                                                                                              Stymne S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plant; plant oil; triglyceride; nutrition; animal feed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99DE-1025718
99DE-1062409
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Pred.
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                                                                                                                                                                                                                                                                                                                                   enase or desaturase, useful for content of unsaturated fatty acids
                                                                                                                                                                                                                                                                                                                                                                                                                              Sperling P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ĎВ
52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Zaehringer U;
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RESULT 12
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Best Local
                                  by (I); (b) an expression cassette (EC) containing (I) linked to one or more regulatory sequences; (c) a vector containing (I) and EC; (d) or ganisms containing (I). EC or the vectors of (c); (e) preparation of unsaturated fatty acids (A) or triglycerides (TG) with increased content of (A) by introducing (I) or EC into an oil-producing organism; (f) protecting (IIa) of 172 aa or 178 aa (given in the specification); (g) production of (A) or TG by using (Ia); and (h) (A) and TG produced by method (g). (I) are used to produce transgenic plants (or other organisms) that produce oils or triglycerides (TG) with increased content of unsaturated fatty acids (A) and to isolate related sequences by homology screening. (A), or TG containing them, are useful in human nutrition (e.g. infant foods), animal feeds, pharmaceuticals and cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can be used to suppress expression of (II), resulting in oils with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ceratodon purpureus.
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                                                                                                                                                                                                                                            activity.
                                                                                                                                                                                                                                                           polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase
                                                                                                                                                                                                                                                                       This invention describes a novel isolated nucleic acid (I) encoding
                                                                                                                                                                                                                                                                                                   Example 8; Page 49-50; 69pp; German.
                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding delta6-acetylenase or desaturase, useful for producing plant oils with increased content of unsaturated fatty acids
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-112150/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Heinz E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BADI ) BASF AG.
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22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-2000; 2000WO-EP05274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Delta6-acetylenase; delta6-desaturase; unsaturated fatty transgenic plant; plant oil; triglyceride; nutrition; an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. purpureus delta6-acetylenase/delta6-desaturase SEQ ID
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|212 hdflh 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conserv
                                                                                                                                                                                                                                            The invention also describes (a) amino acid sequences encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                   Stymne S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   content of
                            content
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99DE-1062409
                         saturated fatty acids
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Pred. No.
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red. No. 55;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sperling
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Sequence

Query Match Best Local S Matches 5

Similarity 5; Conserv

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Score 32; Pred. No.

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RESULT 13
AAB46440
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                 This invention describes a novel isolated nucleic acid (I) encoding polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase activity. The invention also describes (a) amino acid sequences encoded by (I); (b) an expression cassette (EC) containing (I) linked to one or more regulatory sequences; (c) a vector containing (I) and EC; (d) organisms containing (I). EC or the vectors of (c); (e) preparation of unsaturated fatty acids (A) or triglycerides (TG) with increased content of (A) by introducing (I) or EC into an oil-producing organism; (f) proteins (IIa) of I72 and or I78 as (given in the specification); (g) production of (A) or TG by using (Ia); and (h) (A) and TG produced by method (g). (I) are used to produce transgenic plants (or other organisms) that produce oils or triglycerides (TG) with increased content homology screening. (A), or TG containing them, are useful in human polyperiods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding delta6-acetylenase or desaturase, useful for producing plant oils with increased content of unsaturated fatty acids
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Sequence
                                                                                                                                          can be used to suppress expression of (II), resulting
                                                                                                                                                                                       nutrition (e.g. infant foods), animal feeds, pharmaceuticals and cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 7; Page 57-59; 69pp; German
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1999;
22-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-APR-2001
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                                                                                              increased
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 hdfih 216
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                                                                                              content of saturated
520
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99DE-1062409.
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                                                                                                                                                                                                                                                    This invention describes a novel sphingolipid desaturase that selectively clintroduces a double bond into the sphingolase of the ceramide residue of sphingolipids and capnoids. A DNA sequence encoding the sphingolipid content or a vector containing the DNA sequence, can be used to compensed delta-8-unsaturated long-chain base content or an altered content-second delta-8-unsaturated long-chain base cis/trans ratio, especially to compensate for a delta-8-unsaturated long-chain base deficiency, to compensate for a delta-8-unsaturated long-chain base deficiency, to content or an altered content or a delta-8-unsaturated long-chain base deficiency, to compensate for a delta-8-unsaturated long-chain base deficiency, to compensate for a delta-8-unsaturated bases, to increase tolerance content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or content or cont
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                                                                                                                                                              CC (I) by introducing into an organism at least one isolated nucleic acid (II) that encodes a polypeptide (III) with Delta6-desaturase activity. CC Organisms that contain at least 1 wt. 8 (I), on total fatty acid content, CC are then selected. (II) is selected from: (a) a 2012 bp sequence (S1), CC defined in the specification, or its equivalents within the degeneracy of CC the genetic code; or (b) derivatives of the sequence of (a) that encode a CC 525 amino acid polypeptide (S2), defined in the specification, or a CC polypeptide with at least 50% homology with (S2) and practically the same CC enzymatic activity. The invention also describes (I) transgenic organisms CC that contain (II); and (2) oils, lipids and fatty acids produced by the CC enganisms are used in human or animal nutrition, cosmetics, CC pharmaceuticals and agricultural chemicals. (III) can also be used, in CC vitro, for increasing the (I) content of triglycerides. The transgenic CC crganisms have increased contents of (I), or of (I)-containing CC triglycerides, particularly of gamma-linolenic acid.
                                                       Query Match
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Matches 5; Conserv
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Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-834-033A-1
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US-08-33-574-2
US-08-431-080-16
US-08-938-534-16
US-08-946-158A-5
US-08-446-010B-19
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US-08-357-598-6
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US-08-655-574C-9
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US-08-567-508C-2
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2.246 Million cell updates/sec
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Sequence 19, Appli
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      Sequence
14. Appl
16. Appl
16. Appl
17. Appl
18. Appl
19. ```

ALIGNMENTS

## Query Match Best Local Similarity ~+~hes 5; Conserva ; TOPOLOGY: 11; ; MOLECULE TYPE: US-08-834-655-5 RESULT 1 US-08-834-655-5 Sequence 5, Application Patent No. 5968809 TELEX: N/A INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: GENERAL INFORMATION: APPLICANT: KNUTZO REFERENCE/DOCKET NUMBER: 32,750 REFERENCE/DOCKET NUMBER: CGNE.124.00US TELECOMMUNICATION INFORMATION: TELEPHONE: (650) 328-4400 TELEFAX: (650) 328-4477 TELEX: N/A ATTORNEY/AGENT INFORMATION: NAME: RAE-VENTER, BARBARA REGISTRATION NUMBER: 32,7' SOFTWARE: PatentIn Release #1.0, V CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/834,655 FILING DATE: 11-APR-1997 CLASSIFICATION: 435 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk CORRESPONDENCE ADDRESS: ADDRESSEE: RAE-VENTER LAW GROUP, APPLICANT: MURKERJI, PRADIP APPLICANT: HUANG, YUNG-SHENI APPLICANT: THURWOND, JENNIFEE APPLICANT: CHAUDHARY, SUNITA TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS NUMBER OF SEQUENCES: 18 STREET: 260 SHER CITY: PALO ALTO STRANDEDNESS: not relevant COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS COUNTRY: US ZIP: 94306 STATE: ADDRESSEE: RAE-VENTER LAW GROUP, P.C. STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039 LENGTH: amino acid CA 355 amino acids USA THURMOND, JENNIFER CHAUDHARY, SUNITA PatentIn Release #1.0, Version #1.30 KNUTZON, DEBORAH linear peptide US/08834655

Conservative

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Mismatches

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Gaps

0

100.0%;

Score 32; Pred. No.

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Length 355; Indels

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HDFLH 5

US-08-834-033A-6

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밁
 US-09-363-574-5
 US-08-834-033A-6
 Sequence 5, Application US/09363574
 Query Match
Best Local :
 Matches
 Patent No. 6136574
 Sequence
 Sequence 6, Applic Patent No. 6075183
 GENERAL INFORMATION:
APPLICANT: KNUTZO
 APPLICATION NUMBER: US/08/834
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
 NFORMATION FOR SEQ ID NO:
 APPLICANT:
 SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P
STREET: 2001 FERRY BUILDING
 TITLE OF INVENTION:
 APPLICANT:
 MOLECULE TYPE:
 APPLICANT:
 NUMBER OF SEQUENCES:
 TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 APPLICANT:
 APPLICANT:
 11111
70 HDFLH 74
 Local Similarity
mes 5; Conserv
 TELEFAX: (4
 STRANDEDNESS:
 TYPE: amino acid
 COUNTRY: UZIP: 94111
 TOPOLOGY:
 CITY: SAN FRANCISCO
 1 HDFLH 5
 INFORMATION:
 Application US/08834033A
 : KNUTZON, DEBORAH
: MUKERJI, PRADIP
: HUANG, YUNG-SHENG
: THURMOND, JENNIFER
: CHAUDHARY, SUNITA
 CA
 HUANG, YUNG-SHENG
THURMOND, JENNIFER
CHAUDHARY, SUNITA
 MURKERJI, PRADIP
 100.0%; Score 32; DB ilarity 100.0%; Pred. No. 23; Conservative 0; Mismatches
 USA
 (415) 433-8716
 KNUTZON, DEBORAH
 linear
 US/08/834,033A
11-APR-1997
N. ^^~
 peptide
 not relevant
METHODS AND COMPOSITIONS FOR SYNTHESIS
 26
 6:
 CGAB-300.USA
 DB 3; Length 355;
 Indels
 0;
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 0;
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 Query Match
Best Local Similarity
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 TOPOLOGY: 1:
; MOLECULE TYPE:
US-09-363-574-5
 RESULT 4
US-08-834-655-2
 Sequence 2, Application US/08834655 Patent No. 5968809
 GENERAL INFORMATION:
 TELEX: N/A
INFORMATION FOR SEQ ID NO:
 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REGISTRATION NUMBER: CGAE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
 APPLICANT:
APPLICANT:
APPLICANT:
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 CORRESPONDENCE ADDRESS:
ADDRESSEB: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
 MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 ZIP: 94111
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MEDIUM TYPE: Floppy
 TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
 SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
 CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS NUMBER OF SEQUENCES: 18\,
 APPLICANT:
 COUNTRY: U:
ZIP: 94306
 STREET: 260 SHE
 STATE:
 70 HDFLH
 STRANDEDNESS:
 TELEFAX:
 FILING DATE:
 COUNTRY:
 APPLICATION NUMBER: US/09/363,574
 STATE:
 CITY: SAN FRANCISCO
 STREET:
 ADDRESSEE:
 1 HDFLH 5
 amino acid
 CA
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 USA
 HUANG, YUNG-SHENG
THURMOND, JENNIFER
CHAUDHARY, SUNITA
 3: LIMBACH AND LIMBACH L.L.P
2001 FERRY BUILDING
 MURKERJI, PRADIP
 USA
 KNUTZON, DEBORAH
 Conservative
 (415) 433-8716
 linear
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11-APR-1997
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 METHODS AND COMPOSITIONS FOR SYNTHESIS OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS 18
 100.0%;
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 CGAB-202 USA
 Score 32;
Pred. No.
 Mismatches
 4; Length 355;
 Indels
 0;
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CLASSIFICATION:

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Query Match
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vatches 5; Conserve
 Ъ
 MOLECULE TYPE: peptide US-08-834-655-2
 Sequence 4, Application US/08833610 Patent No. 5972664
 -08-833-610-4
 GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
 COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CONTRACT CATTON NUMBER: US/08/833,610
 INFORMATION FOR SEQ ID NO:
 STREET: 200 CITY: PALO ALTO CITY: CALIFORNIA
 APPLICANT:
 REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
 REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)328-4400
 SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
MOLECULE TYPE:
 ATTORNEY/AGENT INFORMATION:
 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION:
 APPLICANT:
 APPLICANT:
 ATTORNEY/AGENT INFORMATION:
 172 HDFLH 176
 APPLICATION NUMBER: FILING DATE: 11-APPLICATION: 439
 TOPOLOGY:
 STRANDEDNESS:
 TELEFAX:
 REGISTRATION NUMBER:
 NAME: RAE-VENTER, BARBARA
 COUNTRY: US
ZIP: 94306
 ADDRESSEE:
 TOPOLOGY:
 STRANDEDNESS:
 TELEFAX:
 1 HDFLH 5
 amino acid
 RAE-VENTER, BARBARA
 E: RAE-VENTER LAW GROUP, P.C. 260 SHERIDAN AVE, P.O. BOX 60039
 HUANG, YUNG-SHENG
THURMOND, JENNIFER
CHAUDHARY, SUNITA
 : (650)328-4400
(650)328-4477
 MURKERJI, PRADIP
 (650) 328-4477
 Conservative
 linear
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 11-APR-1997
N: 435
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 METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
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 100.0%;
 32,750
ER: CGNE.123.00US
 0,
 Score 32;
Pred. No.
 Mismatches
 DB 2; Length 457; 29;
 Indels
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US-08-834-033A-14
; Sequence 14, Application US/08834033A
; Patent NO. 6075183
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
 Ъ
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 RESULT
 US-08-834-033A-2
 US-08-834-033A-2
 Best Loc
Matches
 Query Match
 Patent No.
 Sequence 2, Application US/08834033A Patent No. 6075183
 Matches
 Query Match
Best Local Similarity
 APPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY_AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300.US/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 GENERAL INFORMATION:
 APPLICANT:
APPLICANT:
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
 MOLECULE TYPE:
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES:
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 APPLICANT:
 APPLICANT:
 172 HDFLH 176 ·
 172 HDFLH 176
 Local Similarity hes 5; Conserv
 STREET: 2001 FERKY I
 STRANDEDNESS:
 TELEX:
 TELEFAX:
 COUNTRY:
 STATE:
 1 HDFLH 5
 TOPOLOGY:
 LENGTH:
 ADDRESSEE: LIMBACH AND LIMBACH, L.L.P. STREET: 2001 FERRY BUILDING
 1 HDFLH 5
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 amino acid
 N/A
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 457 amino acids
 (415) 433-8716
 USA
 MUKERJI,
 CHAUDHARY,
 THURMOND, JENNIFER
 KNUTZON,
 Conservative
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 HUANG,
 linear
 peptide
 not relevant
 YUNG-SHENG
 100.0%; Score 32;
100.0%; Pred. No.
tive 0; Mismatch
 DEBORAH
 100.0%; Score 32; DB 100.0%; Pred. No. 29;
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 Mismatches
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 DB 3;
29;
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 Length 457;
 Length 457;
 Indels
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US-09-363-574-2

; Sequence 2, Applic

; Patent No. 6136574
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 ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-834-033A-14
 Matches
 Query Match
Best Local Similarity
 GENERAL INFORMATION:
 APPLICANT:
APPLICANT:
 NFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
 APPLICANT: APPLICANT:
 SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
 REFERENCE/DOCKET NUMBER: CG.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
 APPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
 COMPUTER: 1BM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
 TITLE OF INVENTION:
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
 APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURWOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
 172 HDFLH 176
 STREET: 2001 FERRY CITY: SAN FRANCISCO STATE: CA
 STREET: 2001 FERRY I
 COUNTRY: USA
ZIP: 94111
 TYPE: amino acid
STRANDEDNESS: not
 COUNTRY: UZIP: 94111
 STATE:
 ADDRESSEE:
 ADDRESSEE:
 1 HDFLH 5
 <u>ب</u>
 Application US/09363574
 CA
 CA
 KNUTZON, DEBORAH
MURKERJI, PRADIP
HUANG, YUNG-SHENG
THURMOND, JENNIFER
CHAUDHARY, SUNITA
 E: LIMBACH AND LIMBACH L.L.P.
2001 FERRY BUILDING
 E: LIMBACH AND LIMBACH, L.L.P. 2001 FERRY BUILDING
 USA
 100.0%; ilarity 100.0%; Conservative 0;
 not relevant
 METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
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 CGAB-300.USA
 Score 32; DI
Pred. No. 29
 Mismatches
 DB 3; Length 457;
 Indels
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US-08-431-080-16
; Sequence 16, Application US/08431080
; Patent No. 5698886
 В
 Query Match
Best Local Similarity
Watches 5; Conserva
 ; MOLECULE TYPE: peptide US-09-363-574-2
 RESULT
 APPLICATION NUMBER: US/08/431,080
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SN 08/326,781
FILING DATE: October 20, 1994
CLASSIFICATION: 514
 GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO:
 INFORMATION FOR SEQ ID NO:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS
 NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:155/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
 APPLICANT: Gottschling, Daniel E. APPLICANT: Singer, Miriam S. TITLE OF INVENTION: Telomerase Co
 REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-450
 ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,574
 ATTORNEY/AGENT INFORMATION:
 NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
 SEQUENCE CHARACTERISTICS:
 TELEFAX: (/+-/
 172 HDFLH 176
 STRANDEDNESS: not
 COUNTRY: UN
ZIP: 77210
 STATE:
 CITY: Houston
 TELEFAX:
 FILING DATE:
CLASSIFICATION:
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
 STREET:
 TELEX:
 ADDRESSEE:
 TYPE: amino acid
 1 HDFLH 5
 LENGTH: 457 amino acids
 TEXAS
 P.O. Box 4433
 (415) 433-8716
 UNITED STATES OF AMERICA
 Conservative
 Arnold, White & Durkee
 Concurrently Herewith
 not relevant
 100.0%;
 Telomerase Compositions and Methods
 38,651
 2:
 0;
 CGAB-202 USA
 Score 32;
Pred. No.
 Mismatches
 4; Length 457;
 Indels
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 Query Match
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 RESULT 10
US-08-938-534-16
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 ; TOPOLOGY: US-08-431-080-16
RESULT 11
US-09-046-158A-5
 NAME: Parker, David L.
REGISTRATION NUMBER: 3,165
REFERENCE/DOCKET NUMBER: ARCD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 16:
 Patent No.
 Sequence 16, Application US/08938534 Patent No. 5916752
 Matches
 Query Match
Best Local Similarity
 GENERAL INFORMATION:
 SEQUENCE CHARACTERISTICS:
LENGTH: 582 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
 APPLICANT: Gottschling, Dani
APPLICANT: Singer, Miriam S.
TITLE OF INVENTION: Telomera
 APPLICATION NUMBER: SN 08/326,781 FILING DATE: October 20, 1994 ATTORNEY/AGENT INFORMATION:
 MEDIUM TYPE: Floppy
 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
 CURRENT APPLICATION DATA:
 PRIOR APPLICATION DATA:
 343 HDFLH 347
 343 HDFLH 347
 STATE: T
 FILING DATE: 26-SEP-1997
CLASSIFICATION: 536
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.30
 STREET: P.O. B
CITY: Houston
 APPLICATION NUMBER: 08/431,080 FILING DATE:
 APPLICATION NUMBER:
 TYPE: amino acid
STRANDEDNESS: si
 ADDRESSEE: Arnold, White & Durkee
 1 HDFLH 5
 1 HDFLH 5
 5; Conservative
 77210
 TEXAS
 P.O. Box 4433
 UNITED STATES OF AMERICA
 Conservative
 Gottschling, Daniel E.
 linear
 Floppy disk
 single
 Telomerase Compositions and Methods
 100.0%;
 100.0%; Score 32;
100.0%; Pred. No.
 US/08/938,534
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 Indels
 0
 0;
 Gaps
 0;
 0;
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밁
 ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-046-158A-5
 US-08-446-038B-19
 RESULT 12
 Sequence 19, Application US/08446038B Patent No. 5658791 GENERAL INFORMATION:
 Sequence 5, Application US/09046158A Patent No. 6187552
 Matches
 Query Match
Best Local Similarity
 GENERAL INFORMATION:

APPLICANT: Roberds, Steven L.

APPLICANT: Kaytes, Paul S.

TITLE OF INVENTION: METHOD FOR IDENTIFYING INHIBITORS OF TITLE OF INVENTION: JAK2/CYTOKINE RECEPTOR BINDING NUMBER OF SEQUENCES: 30
 TELEX: 224401
INFORMATION FOR SEQ ID NO:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
 APPLICANT: Wilks, Andrew F.; Ziemiecki, Andrew;
APPLICANT: Harpur, Ailsa
TITLE OF INVENTION: No. 5658791el Protein Tyrosine Kinase
NUMBER OF SEQUENCES: 23
 SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acid
 NAME: Darnley Jr., James D. REGISTRATION NUMBER: 33,673 TELECOMMUNICATION INFORMATION:
 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 CORRESPONDENCE ADDRESS:
SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
 ADDRESSEE: Felfe & I
 TELEFAX: v...
TELEFAX: 224401
 159 HDFVH 163
 ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
 TELEPHONE: 616/833-8897
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 STATE:
 FILING DATE:
 COUNTRY: U
 STATE:
 ADDRESSEE: Pharmacia & Upjohn Co., ADDRESSEE: Legal Services STREET: 301 Henrietta Street
 OPERATING SYSTEM:
 ZIP: 10022
 STRANDEDNESS:
 CITY: Kalamazoo
 COUNTRY:
 APPLICATION NUMBER: US/09/046,158A
 1 HDFLH 5
 4;
 amino acid
 MI
 New York
 294 amino acids
 USA
 USA
 Conservative
 616/833-2210
 single
 90.6%;
 PC-DOS
 1; Mismatches
 Score 29;
Pred. No.
 DB 4;
 Intellectual Property
 0
 Length 294;
 Indels
 0
 Gaps
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PRIOR APPLICATION DATA:

FILING DATE:

APPLICATION NUMBER: US/08/446,038B

19-MAY-1995

APPLICATION NUMBER: CLASSIFICATION:

08/064,067

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Вb
 US-08-446-010B-19
 US-08-446-038B-19
 Query Match
Best Local Similarity
Matches 4; Conserv
 Sequence 19,
 Sequence 19, Application US/08446010B Patent No. 5716818
GENERAL INFORMATION:
 TELEPHONE: 212-688-920
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 APPLICATION DATA:
FILING DATE: 19-may.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,067
APPLICATION NUMBER: 30-Jun-1993
 CLASSIFICATION: 433
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,038
FILING DATE: 19-May-1995
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
 SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS
 APPLICANT: Wilks, Andrew F.; Ziemiecki, Andrew;
APPLICANT: Harpur, Ailsa
TITLE OF INVENTION: No. 5716818el Protein Tyrosine Kinase
 REFERENCE/DOCKET NUMBER: LUTELECOMMUNICATION INFORMATION: 212-688-9200
 APPLICATION NUMBER: Australian 88229/91
FILING DATE: 27-No. 5558791-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5558791man D.
REGISTRATION NUMBER: 30,946
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: Australian PK3594/90
FILING DATE: 28-No. 5658791-1990
PRIOR APPLICATION DATA:
 NUMBER OF SEQUENCES:
 COMPUTER: IBM PS/
OPERATING SYSTEM:
 APPLICATION NUMBER:
 APPLICATION NUMBER: US/08/446,010B
FILING DATE: 19-May-1995
 CITY: New York City
STATE: New York
 16 HDFVH 20
 LENGTH: 971 amino acids TYPE: amino acid
 APPLICATION NUMBER: PCT/US91/08889 FILING DATE: 26-No. 5658791-1991
 COUNTRY:
 STREET:
 FILING DATE:
 ADDRESSEE:
 1 HDFLH 5
 COPOLOGY:
 10022
 4; Conservative
 E: Felfe & Lynch
805 Third Avenue
 USA
 linear
 IBM PS/2
 Diskette, 3.5
 30-Jun-1993
MBER: PCT/US91/08889
26-No. 5716818-1991
 90.6%;
 PC-DOS
 1; Mismatches
 Score 29; DB 1;
Pred. No. 2.3e+02;
 inch, 360 kb storage
 DB 1; Length 971;
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 US-08-805-445-19
 RESULT
 US-08-446-010B-19
 Query Match
Best Local S
 Sequence 19, Application US/08805445 Patent No. 5821069
 Matches
 GENERAL INFORMATION:
 TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO:
 FILING DATE: 27-NO. JULIUS ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5821069man D.
NAME: 30,946
 FILING DATE: 30-Jun-1993
APPLICATION NUMBER: PCT/US91/08889
FILING DATE: 26-No. 5821069-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: Australian PK3594/90
FILING DATE: 28-No. 5821069-1990
PRIOR APPLICATION DATA:
 CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
 CORRESPONDENCE ADDRESS:
 APPLICANT: Harpur, Ailsa TITLE OF INVENTION: No. 5 NUMBER OF SEQUENCES: 23
 APPLICANT:
 SEQUENCE CHARACTERISTICS:
LENGTH: 971 amino acid
 ATTORNEY/AGENT INFORMATION: NAME: Baer, Madeline F.
 PRIOR APPLICATION DATA:
TELECOMMUNICATION INFORMATION:
 PRIOR APPLICATION DATA:
 TELECOMMUNICATION INFORMATION:
 NUMBER OF SEQUENCES:
 OPERATING SYSTEM: PC-I
SOFTWARE: Wordperfect
 FILING DATE: 25
CLASSIFICATION:
 REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
 APPLICATION NUMBER: Australian 88229/91 FILING DATE: 27-No. 5821069-1991
 FILING DATE: 19-MAY-1995
APPLICATION NUMBER: 08/064,067
 COUNTRY:
 STREET: 805 Third Avenue CITY: New York City
 16 HDFVH 20
 Local Similarity
nes 4; Conserv
 TYPE: amino acid
 APPLICATION NUMBER: Australian 88229/91 FILING DATE: 27-No. 5716818-1991
 APPLICATION NUMBER: FILING DATE: 28-No.
 APPLICATION NUMBER:
 APPLICATION NUMBER:
 REFERENCE/DOCKET NUMBER:
 REGISTRATION NUMBER:
 TOPOLOGY:
 JECUPANCE: 212-00 FELEPHONE: 212-838-3884
 ADDRESSEE:
 1 HDFLH 5
 10022
 New York
 Wilks, Andrew F.; Ziemiecki, Andrew;
 USA
 Conservative
 linear
 IBM PS/2
 Felfe & Lynch
 212-688-9200
 25-FEB-1997
 19-MAY-1995
 Diskette, 3.5 inch, 360 kb storage
 PC-DOS
 90.6%;
 30,946
 Australian PK3594/90
5716818-1990
 36,437
 5821069el Protein Tyrosine Kinase
 19:
 LUD 5244.3
 Score 29; I
Pred. No. 2.
 Mismatches
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 DB 1;
 Length 971;
 Indels
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Query Match
Best Local Similarity
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 TOPOLOGY: US-08-805-445-19
 US-08-064-067D-19
 US-08-064-067D-19
 TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 971 amino acids
TYPE: amino acid
TYPE: amino acid
 Query Match
Best Local Similarity
Matches 4; Conserv
 Sequence 19, Application US/08064067D Patent No. 5852184
 APPLICATION UNBER: PCT/US91/08889
FILING DATE: 26-No. 5852184-1991
PRIOR APPLICATION DATA:
APPLICATION UNBER: Australian PK3594/90
FILING DATE: 28-No. 5852184-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: Australian 88229/91
FILING DATE: 27-No. 5852184-1991
FILING DATE: 27-No. 5852184-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5852184-1991
ATTORNEY/AGENT UNUMBER: 30,946
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: LUD 5244
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
TELEPAX: 212-688-9200
 GENERAL INFORMATION:
 TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 971 amino acid
 SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/064,067D
FILING DATE: 30-Jun-1993
PRIOR APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
 APPLICANT: Wilks, Andrew F.; Ziemiecki, Andrew;
APPLICANT: Harpur, Ailsa
TITLE OF INVENTION: No. 5852184el Protein Tyrosine Kinase
 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
 STREET: 805 Third Avenue CITY: New York City STATE: New York
 COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
 16 HDFVH 20
16 HDFVH 20
 COUNTRY: U
 STREET:
 TYPE: amino acid
 ADDRESSEE:
 1 HDFLH 5
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 971 amino acids
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 USA
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 linear
 Felfe & Lynch
 3: NO.
 90.6%;
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 19:
 1; Mismatches
 Score 29; DB 2; Le pred. No. 2.3e+02; 1; Mismatches 0;
 Score 29; DB 2;
Pred. No. 2.3e+02;
 0; Indels
 Length 971;
 Length 971;
 Indels
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Search completed: August 9, 2001, 20:25:07 Job time: 206 sec

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| <b>T</b>                                                                                                                                                                                                                        | ***       | *        | ŵ-                                   | •         | v        | •          |
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| <b>e</b><br>•                                                                                                                                                                                                                   |           |          |                                      |           |          | ***        |
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| <i>•</i>                                                                                                                                                                                                                        |           |          | *.                                   |           |          | • .        |
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| ਹੈ:<br>ਜੋ                                                                                                                                                                                                                       |           |          |                                      |           |          |            |
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| ±.,                                                                                                                                                                                                                             |           |          |                                      |           |          |            |
| <b>A.</b> 8                                                                                                                                                                                                                     | , protein | 477      | <i>x</i> • •                         | *         |          |            |
|                                                                                                                                                                                                                                 |           |          |                                      |           |          |            |
| 。<br>表<br>概                                                                                                                                                                                                                     |           |          |                                      |           |          |            |
| Υ .<br>3-                                                                                                                                                                                                                       |           |          |                                      |           |          |            |
|                                                                                                                                                                                                                                 |           |          | •                                    |           |          |            |
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Result
No.
 Post-processing: Minimum Match 0% Maximum Match 10
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 Title:
Perfect score:
 Run
 Database :
 Total number of hits satisfying chosen parameters:
 Searched:
 Scoring table:
 Sequence:
 OM protein - protein search, using sw model
 on:
 3209884
3320984
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Score
 Query
Match Length DB
\begin{array}{c} 993 \\ 900 \\
 SwissProt_39:*
 93435 seqs,
 BLOSUM62
Gapop 10.0 ,
 US-09-367-013B-2_COPY_172_176
32
 Listing first 45 summaries
 August 9, 2001, 20:36:49;
 1 HDFLH
 Copyright
GenCore version 4.5 (c) 1993 - 2000 Com
 34255486 residues
 Gapext 0.5
 100%
 JAK2_HUMAN
JAK2_RAT
YGE1_YEAST
RISB_BRUAB
YE99_MYCPN
Y038_NPVOP
BZTD_RHOCA
TREC_BCCLI
TREC_BCSLI
TREC_BCSU
MEPB_HUMAN
MEPB_HUMAN
MEPB_RAT
CIN6_HUMAN
CIN2_HUMAN
CIN2_HUMAN
IBB2_PHAAN
IBB2_PHAAN
IBB2_PHAAN
IBB2_CHOCR
CPC1_CANPG
GLBY_CHITP
CB1H_SALTY
COQ4_YEAST
 DMPN_PSESP
YX23_CAEEL
P4HA_CAEEL
VE1_HPV41
YKF0_YEAST
 MVIM_SALTY
JAK2_MOUSE
 YBBB_ECOLI
045B_DROME
 SUMMARIES
 Search time 28.86 Seconds (without alignments) 5.935 Million cell updates/sec
 Compugen Ltd
 030207 archaeoglob
P37168 salmonella
052120 mus musculu
060674 homo sapien
062689 rattus norv
P53182 saccharomyc
Q44668 brucella ab
P75288 mycoplasma
 P54323
P81580
P18968
P18969
Q05590
P91428
O13525
P33667
P33667
P197389
P197389
P19739
Q111194
Q11576
P27551
 P28826
Q01118
 Q16820
Q61847
 Q05125
Q52666
 Description
 5 bacillus su
6 homo sapien
7 mus musculu
5 rattus norv
8 homo sapien
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1 phaseclus a
1 chancer pagu
2 chironomus
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caenorhabdi
saccharomyc
saccharomyc
rescherichia
drosophila
pseudomonas
caenorhabdi
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human papil
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bacillus su
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rhodobacter
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TYK2\_HUMAN

В Q

56 HDFIH

60

1 HDFLH 5

Query Match Best Local S Matches 4

Local Similarity 80. nes 4; Conservative

93.8%;

Score 30; DB Pred. No. 22; 1; Mismatches

1; 0

Length 371; Indels

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Gaps

| S K D D C C C C C C C C C C C C C C C C C                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | RA RA RA RA RA RA RA RA RA RA RA RA RA R                                                                                                                                                                                                                                                                                                                                                                                                                                      | OC OC OC OC OC OC OC OC OC OC OC OC OC O                                                                                                                                                                                                                                                                            | RESU<br>Y028<br>ID<br>AC<br>DT<br>DT<br>DT                                           |                                                                                                                                     |
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| This SWIS between the Europ use by modified entities or send a EMBL; AEC TIGR; AFF Hypotheti SEQUENCE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Kirkness<br>Kirkness<br>Peterson<br>Overbeek<br>Cotton M<br>Sadow P.I<br>Mason J.J<br>Venter J<br>Venter J<br>Venter Gom<br>reducing<br>Nature SIMI                                                                                                                                                                                                                                                                                                                           | Archaeogl<br>Archaeogl<br>Archaeogl<br>Archaeogl<br>NCBI_Taxl<br>[1]<br>SEQUENCE<br>STRAIN-VC<br>MEDLINE-STRAIN-VC<br>MEDLINE-STRAIN-VC<br>MEDLINE-STRAIN-VC<br>MEDLINE-STRAIN-VC                                                                                                                                   | 1 -                                                                                  | 00000044444400000000000000000000000000                                                                                              |
| This SWISS-PROT between the Swi the European Bio use by non-promodified and thin entitles require entitles require or send an email EMBL; AE001105; TIGR; AF0028;EMBL; AE001105; SEQUENCE 371 A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | KITKNESS E.F., Peterson S. Re Overbeek R., Go Cotton M.D., Sp Sadow P.W., D'A Mason T.M., Ols Venter J.C.; "The complete g "The complete g reducing archae Nature 390:3641- SIMILARITY: MTH1067 AND                                                                                                                                                                                                                                                                           | Archaeoglobus<br>Archaeoglobus<br>Archaeoglobus<br>NCBI_TaxID=223<br>[1]<br>SEQUENCE FROM<br>STRAIN=VC-16<br>STRAIN=VC-16<br>MEDLINE-980493<br>MEDLINE-980493<br>Klenk HP., C<br>Ketchum K.A.,<br>Ketchum K.A.,                                                                                                     | T 1 ARCFU Y028_ARCFU 030207; 030207; 15-JUL-1998 15-JUL-1998 15-JUL-1998 15-JUL-1998 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                               |
| the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the Swiss IT the S | SS E.F. Dougherty son S. Reich C.I., sek R. Gocayne J.D. P.W. Gocayne J.D. T.M. D. Spriggs T. T.M. Olsen G.J., c J.C.; c J.C.; complete genome seq ing archaeon Archae s 390.364-370(1997) IMILARITY: STRONG, FHILORY AND A.FULGID FHILORY AND A.FULGID                                                                                                                                                                                                                       | iobus fulgidus. Euryarchaeota; Euryarchaeota; Lo-2234; FROM N.A. FROM N.A. FROM 9304; PubMe 8049343; PubMe 8049343; PubMe 10. Clayton R. (.A., Dodson R. Onack                                                                                                                                                      | (Re<br>(Re<br>(PR                                                                    | 81.2<br>81.2<br>81.2<br>81.2<br>81.2<br>81.2<br>81.2                                                                                |
| entry is copies Institute oinformatics offit institution is statement as a license of to license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license of the license | Kirkness E.F., Dougherty B.A., McK<br>Peterson S., Reich C.I., McNeil L.<br>Overbeek R., Gocayne J.D., Weidann<br>Cotton M.D., Spriggs T., Artiach F<br>Sadow P.W., D'Andrea K.P., Bowman<br>Mason T.M., Olsen G.J., Fraser C.M<br>Venter J.C.;<br>"The complete genome sequence of t<br>reducing archaeon Archaeoglobus fu<br>Nature 390:364-370(1997).<br>"I SIMILARITY: STRONG, TO M.JANNA<br>MTH1067 AND A.FULGIDUS AF0181.                                               | Archaeoglobus fulgidus. Archaeoglobus fulgidus. Archaeoglobus. Archaeoglobus. NCBI_TaxID=2234; [1] SEQUENCE FROM N.A. STRAIN=VC-16 / DSM 4304 / ATCC MEDLINE-98049343; PubMed=938947 Klenk HP., Clayton R.A., Tomb Ketchum K.A., Dodson R.J., Gwin Richardson D.L., Kerlavage A.R. Fleischmann R.D., Onackenbush I. | STANDARD; I<br>1. 36, Created)<br>1. 36, Last sequ<br>1. 36, Last anno               | 1123<br>1146<br>1146<br>1160<br>201<br>201<br>201<br>201<br>201<br>201<br>201<br>201<br>201<br>20                                   |
| copy<br>cute<br>cute<br>isitut<br>int i<br>int i<br>inseei                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | MCI<br>MCI<br>Art<br>Art<br>Pras                                                                                                                                                                                                                                                                                                                                                                                                                                              | rch                                                                                                                                                                                                                                                                                                                 | eate<br>st s<br>3t s                                                                 | 4444444444                                                                                                                          |
| yright. It is produc of Bioinformatics of Bioinformatics Institute. There as it is not removed. Usa agreement (See http: isb-sib.ch).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Dougherty B.A. McKenney K., Adams M.D., Loftus B. eich C.I., McNeill L.K., Badger J.H., Glodek A., Zho ocayne J.D., Weidman J.F., McDonald L., Utterback T priggs T., Artlach P., Kaine B.P., Sykes S.M., Andrea K.P., Bowman C., Fujli C., Garland S.A., sen G.J., Fraser C.M., Smith H.O., Woese C.R., sen G.J., Fraser the hyperthermophilic, sulphate-eon Archaeoglobus fulgidus.*;  -370(1997)  T. STRONG, TO M.JANNASCHII MJ1678, M.THERMOAUTOTROPH DA.FULGIDUS AF0181. | glc<br>5;<br>5;                                                                                                                                                                                                                                                                                                     | PRT; 371 AA.  ted) sequence update) annotation update)                               | PHFS_DESVH F802_SCHMA HBB_ALLMI Y4LN_RHISN ARA5_ARAHY PSPA_HUMAN COAT_PYMVV YURL_BACSU YHG2_YEAST LG1_MAIZE TRPB_CAUCR XYLA_THEET   |
| d the EMBL outs no restrictions content is in by and for co www.isb-sib.ch/a                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | M.D. Loftus B. Glodek A. Zh L. Utterback Sykes S.M. aarland S.A. Woese C.R., hillic, sulphate                                                                                                                                                                                                                                                                                                                                                                                 | lobaceae; lobaceae; Nelson K.E., Peterson J. Peterson J. A. G. G. G. H.                                                                                                                                                                                                                                             |                                                                                      | P07603<br>P16464<br>P02130<br>P5554449<br>P07714<br>P07714<br>P27255<br>P27255<br>P27255<br>P27259<br>P27259<br>P27259              |
| ed through a collaboration and the EMBL outstation - e no restrictions on its s content is in no way ge by and for commercial //www.isb-sib.ch/announce/                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | IS M.D., LOTTUS B., I., Glodek A., Zhou L., d. L., Utterback T., Sykes S.M., Garland S.A., Woese C.R., philic, sulphate- M.THERMOAUTOTROPHICUM                                                                                                                                                                                                                                                                                                                                | D .                                                                                                                                                                                                                                                                                                                 |                                                                                      | desulfovibr schistosoma alligator m rhizobium s arachis hyp homo sapien potato yell bacillus su sea mays (m caulobacter thermoanaer |

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RESULT 2
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ID MVIM_SALTY
AC P37168;
 RESULT 3
JAK2_MOUSE
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 Query Match
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 JAK2_MOUSE STANDARD;
Q62120; Q62124;
Q1-NOV-1997 (Rel. 35, Cree
01-NOV-1997 (Rel. 35, Last
15-JUL-1999 (Rel. 38, Last
TYROSINE-PROTEIN KINASE JI
 CONFLICT
 Virulence.
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 SEQUENCE FROM N.A. STRAIN=LT2 / KK1004; van Slooten J.-C., O
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
[1]
 Mus musculus (Mouse)
 EMBL; Z26133; CAA81133.1; -. EMBL; D25292; BAA04981.1; -.
 flgN.";
Gene 143:49-54(1994)
 Salmonella typhimurium,
 "Sequence analysis of the
 van Slooten J.-C., Okada T., Kutsukake K., Pechere J.-C., Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases.
 Salmonella
 Bacteria; Proteobacteria;
 Salmonella typhimurium
 VIRULENCE FACTOR MVIM.
 01-OCT-1994
01-NOV-1997
 01-OCT-1994
 Pfam; PF01408; GFO_IDH_MocA;
 StyGene; SG10239;
 MEDLINE=94259301;
 SEQUENCE FROM N.A.
 NCBI_TaxID=602;
 163
 nterPro;
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 SIMILARITY: TO E.COLI MVIM
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 S40270; S40270
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 Similarity
 IPR000683; -
 167
 Ç,
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307
 (Rel.
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 Conservative
 A,
 STANDARD;
 35,
 PubMed=8200538;
da T., Yokoseki T., Iino T.;
s of the flgA gene and its adjacent region in
urium, and identification of another flagellar gene,
 mviM.
 163
194
33958
 Okada T.,
 90.6%;
 Last sequence update)
Last annotation update)
SE JAK2 (EC 2.7.1.112) (JANUS
 'Created)
 Last sequence up
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 Score 29; DB
Pred. No. 29;
1; Mismatches
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 Craniata; Vertebrata; Sciurognathi; Muridae;
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-> E (IN REF. 2)
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 subdivision;
 update)
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 DB
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 AA
 Enterobacteriaceae,
 0;
 Length 307;
 CRC64;
 Indels
 KINASE
 Euteleostomi;
 2) (JAK-2).
 Harayama
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 Gaps
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Best Loc
Matches
 Query Match
 PROSITE; PS00107; PROTEIN_K
PROSITE; PS00109; PROTEIN_K
PROSITE; PS500111
 MOD_RES
CONFLICT
CONFLICT
CONFLICT
 BINDING
ACT_SITE
 DOMAIN
 SEQUENCE OF 973-1043 FROM N.A. MEDILINE-90152381; PubMed-2482828; Wilks A.F., Kurban R.R., Hovens C.M., Ra "The application of the polymerase chain of the protein tyrosine kinase family."; Gene 85:67-74(1989).
 SH2
 EMBL; L16956; AAB41327.1; -. EMBL; M33423; AAA40014.1; -. HSSP; P11362; 1FGI.
 Transferase;
 InterPro; IPR000719; -.
InterPro; IPR000980; -.
InterPro; IPR001245; -.
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 MEDLINE=89160824;
Wilks A.F.;
 interleukin 3 signal transduction. Proc. Natl. Acad. Sci. U.S.A. 90:8
 Silvennoinen O., Witthuhn
 SEQUENCE
 DOMAIN
 DOMAIN
 PROSITE;
 modified and this statement is not removed.
 the polymerase chain reaction.
 "Two putative protein-tyrosine kinases identified
 "Structure of the murine Jak2 protein-tyrosine kinase interleukin 3 signal transduction.";
 Ihle J.N.;
 MEDLINE=93391367; PubMed=8378315;
 Local
 DOMAIN 1.
SIMILARITY: WITH NONRECEPTOR
BELONGS TO THE JANUS KINASES
 DOMAIN: POSSESSES TWO PHOSPHOTRANSFERASE DOMAINS. THE SECOND ONE PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE PRESENCE OF SLIGHT DIFFERENCES SUGGEST A DIFFERENT ROLE FOR
 domain;
 SUBCELLULAR LOCATION: WHOLLY INTRACELLULAR,
 ASSOCIATED (BY SIMILARITY)
 MGI:96629;
 Similarity 80.4; Conservative
 PS50001;
 OF 973-1043 FROM N.A.
 401
545
849
855
882
976
1007
1016
1024
 Repeat
 Tyrosine-protein
 ξ
 PROTEIN_KINASE_ATP;
 1043
 482
809
1124
863
863
882
976
1007
1016
 SH2;
 PubMed=2466296;
 PROTEIN_KINASE_TYR;
PROTEIN_KINASE_DOM;
 90.6%;
 130260
 UNKNOWN_1
 B.A.,
 PHOSPHORYLATION (AUTO-) (BY : S -> R (IN REF. 2 AND 3). Q -> E (IN REF. 2 AND 3). VV -> IP (IN REF. 2 AND 3). WW: 746CD480EB0A21B9 CRC64;
 Score 29; DB
Pred. No. 1.2e
1; Mismatches
 SH2 (ATYPICAL).
PROTEIN KINASE 1.
PROTEIN KINASE 2.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
 X.
 PROTEIN KINASE
ATP (BY SIMILAR
ATP (BY SIMILAR
BY SIMILARITY.
 90:8429-8433(1993)
 kinase;
 Quelle F.W., Cleveland J.L.,
 SUBFAMILY.
 TYPE TYROSINE-PROTEIN KINASES
. 1.2e+02;
0;
 ATP-binding;
 Ralph S.J.;
ain reaction
 DB 1;
 Usage
 Length 1129;
 POSSIBLY MEMBRANE
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 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-98289582; PubMed-9618263;
MEDLINE-98289582; PubMed-9618263;
 JAK2_HUMAN STANDARD; PRT; 1132 AA. 060674; 075297; 014636; 15-DEC-1998 (Rel. 37, Created) 01-OCT-2000 (Rel. 40, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) TYROSINE-PROTEIN KINASE JAK2 (EC 2.7.1.112) (JANUS KINASE 2) (JAK-2).
 use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
 -i- FUNCTION: TYROSINE KINASE OF THE NON-RECEPTOR TYPE,
INTERLEUKIN 3 SIGNAL TRANSDUCTION.
-i- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP
 Dalal I., Arpaia E., Dadi H., "Cloning and characterization Blood 91:844-851(1998).
 "Cloning and characterization of human Jak-2 kina expression in immune cells and muscle tissue."; Biochem. Biophys. Res. Commun. 246:627-633(1998).
 t(9;15;12) in a myeloid leukemia.
Blood 90:2535-2540(1997).
 Peeters P., Raynaud S.D., Cools J., Wlodarska Philip P., Monpoux F., Van Rompaey L., Baens
 SEQUENCE FROM N.A. MEDLINE=97465498; PubMed=9326218;
 Saltzman A., Stone M.,
Ivashchenko Y.;
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 InterPro;
 InterPro;
 MIM; 147796;
 the European Bioinformatics Institute.
 associated kinase
 MEDLINE-98118198;
 SEQUENCE FROM N.A.
 Homo sapiens (Human).
 "Fusion of
 159
 DOMAIN 1.

DISEASE: A FORM OF
BY A CHROMOSOMAL 1
ETV6 AND JAK2.

SIMILARITY: WITH N
 SUBCELLULAR INC.

ASSOCIATED (BY SIMILARITY).

ASSOCIATED (BY SIMILARITY).

DOMAIN: POSSESSES TWO PHOSPHOTRANSFERASE DOMAINS. THE PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY)

PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY)

ROBERT OF STRING DIFFERENCES SUGGEST A DIFFERENT ROI
 BELONGS
 SUBCELLULAR LOCATION: WHOLLY INTRACELLULAR, POSSIBLY MEMBRANE
 PROTEIN TYROSINE PHOSPHATE
 SWISS-PROT entry is copyright. It is produced through a collaboration -
 HDFVH
 AF001362;
AF005216;
 AF058925;
 an email to license@isb-sib.ch).
 IPR000719;
 TEL, the ETS-variant gene 6 (ETV6), kinase JAK2 as a result of t(9;12)
 163
 TO THE JANUS KINASES
 AAC23982.1; -.
AAC23653.1; -.
AAB82092.1; -.
 PubMed=9446644;
 OF PRE-B ACUTE
 Chordata;
Primates;
 S.D., Cools J., Wlodarska I.,
 Kulkarni S., of the human
 Craniata; Vo
Catarrhini;
 Bioinformatics
 TYPE TYROSINE-PROTEIN KINASES SUBFAMILY.
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 MYELOID LEUKEMIA T(9;12)(P24;P13)
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mouse Jak2.";
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 JAK2_RAT
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 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TYROSINE-PROTEIN KINASE JAK2 (EC 2.7.1.112) (JANUS KINASE
 PROSITE; PS50001; SH2; UNKNOWN_1.

PROSITE; PS50001; SH2; UNKNOWN_1.
 -i- FUNCTION: TYROSINE KINASE OF THE NON-RECEPTOR T
INTERLEUKIN 3 SIGNAL TRANSDUCTION.
-i- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -
PROTEIN TYROSINE PHOSPHATE.
-i- SUBCELLULAR LOCATION: WHOLLY INTRACELLULAR, POS
 "Cloning of the gene encoding Gene 158:281-285(1995).
 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 ÷
 MEDLINE=95331631; PubMed=7607555; Duhe R.J., Rui H., Greenwood J.D.,
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 DOMAIN
 SEQUENCE FROM N.A.
 Rattus norvegicus
 JAK2
 NP_BIND
 DOMAIN
 DOMAIN
 NCBI_TaxID=10116;
 159 HDFVH 163
 1 HDFLH
 ASSOCIATED (BY SIMILARITY).
TISSUE SPECIFICITY: HIGHLY ABUNDANT IN
ABUNDANT IN SKELETAL MUSCLE AND TESTIS,
 HEART, LUNG AND LIVER.

DOMAIN: POSSESSES TWO PHOSPHOTRANSFERASE DOMAINS. THE SECOND PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE PRESENCE OF SLIGHT DIFFERENCES SUGGEST A DIFFERENT ROLE FOR
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 domain;
 BELONGS
 SIMILARITY:
 PF00069;
 Similarity 80.0
4; Conservative
 PS00107; PROTEIN_KINASE_ATP; PS00109; PROTEIN_KINASE_TYR;
 Repeat;
401
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1007
1007
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1132 AA;
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 TO THE JANUS KINASES
 pkinase; 2.
 STANDARD;
 (Rat).
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1207
 Chordata;
Rodentia;
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 90.6%;
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 ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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BY SIMILARITY.
CHOSPHORYLATION (AUTO-) (
P->S (IN REF. 1).
I -> V (IN REF. 2).
MW: C30669EF1A7DA80C CRC6
 1;
 WW;
 Score 29;
Pred. No.
 PROTEIN KINASE 1. PROTEIN KINASE 2.
 SH2 (ATYPICAL)
 rat JAK2,
 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
 PRT;
 Mismatches
 translocation;
 TYPE TYROSINE-PROTEIN KINASES SUBFAMILY.
 Garvey
JAK2, a
 1132
 ; DB 1;
. 1.2e+02;
 ATP-binding; Phosphorylation;
 211
 Å
 K., Farr
protein
 BRAIN AND SPLEEN,
 AND
 0
 Farrar W.L.;
 Length 1132
 Proto-oncogene
 DETECTABLE
 POSSIBLY MEMBRANE
 CRC64;
 TYPE,
 tyrosine kinase.";
 Indels
 ADP
 Murinae; Rattus
 (BY SIMILARITY).
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 2) (JAK-2).
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RESULT 6
YGE1_YEAST
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 Query Match
Best Local S
Matches 4
 InterPro; IPR000980; -.
InterPro; IPR001245; -.
Pfam; PF00017; SH2; 1.
Pfam; PF00069; pkinase; 2.
PROSITE; PS00107; PROTEIN_KINASE_ATD; 1
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1
PROSITE; PS50011; PROTEIN_KINASE_DOM; 2
 01-OCT-1996 (Rel. 3
01-OCT-1996 (Rel. 3
01-NOV-1997 (Rel. 4
HYPOTHETICAL 12.0
 YGE1_YEAST
P53182;
 MOD_RES
SEQUENCE
 NP_BIND
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 DOMAIN
DOMAIN
 EMBL;
 entities requires a license agreement (son send an email to license@isb-sib.ch).
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 SEQUENCE OF 18-104 FROM N.A.
Hebling U., Hofmann B., Delius H.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
 Feuermann M., de Montigny J., Potier S., Souciet J.-L.; "The characterization of two new clusters of duplicated genes suggests a 'Lego' organization of the yeast Saccharomyces cerchromosomes.";
 Eukaryota; Fungi;
Saccharomycetales;
 Saccharomyces cerevisiae (Baker's yeast).
 SH2 domain;
 TRANSMEM
 Hypothetical
 MEDLINE-97377993;
 SEQUENCE FROM N.A.
 NCBI_TaxID=4932;
 DOMAIN
 Transferase;
 PROSITE;
 ACT_SITE
 nterPro;
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 159 HDFVH 163
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European Bioinformatics Institute. There are no restrictions on it
by non-profit institutions as long as its content is in no wa
 SWISS-PROT entry is copyright. It is produced through a collaboration -
 HDFLH 5
 : Z72563; CAA96743.1; -. S0003009; YGL041C.
 13:861-869(1997).
 Similarity
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 requires a license agreement (See
 PS50001; SH2;
 104
 Repeat.
401
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849
882
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 protein;
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 Tyrosine-protein
 83
 Ã,
 STANDARD;
 AA;
 34,
35,
35,
 PubMed=9234674;
 Ascomycota;
 1007
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1126
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 11977
 90.6%;
 130585
 ; UNKNOWN_1.
 Transmembrane
 Last sequence update)
Last annotation update)
PROTEIN IN DST1-HEM2 IN
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 MW;
 Score 29; DB Pred. No. 1.2e 1; Mismatches
 SH2 (ATYPICAL).
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 PHOSPHORYLATION (AUTO-) (BY W; C3AEDF2FECE8B95A CRC64;
 Saccharomycotina;
 PRT;
85A3E9FC9AE7AD93 CRC64;
 104
 ATP-binding; Phosphorylation;
 DB 1;
1.2e+02;
 Saccharomyces
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 INTERGENIC REGION
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 RESULT 7
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 01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
6,7-DIMETHYL-8-RIBITYLLUMAZINE SYNTHASE (EC 2.5.1.9) (DMRL SYNTHASE)
(LUMAZINE SYNTHASE) (RIBOFLAVIN SYNTHASE BETA CHAIN).
 EMBL; Z46864; CAA86936.1; -. Pfam; PF00885; DMRL_synthase;
 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
 Hemmen F., Weynants V., Scarcez T., Letesson J., Saman E.; "Cloning and sequence analysis of a newly identified Brucella abortus gene and serological evaluation of the 17-kilodalton antigen that it
 Brucella abortus
 044668;
 RISB_BRUAB
 Riboflavin
 use by non-profit institutions as long modified and this statement is not removed
 the European
 - ! - SIMILARITY: BELONGS TO THE DMRL SYNTHASE FAMILY.
 encodes."
 MEDLINE=95393285;
 SEQUENCE FROM N.A
 NCBI_TaxID=235;
 Brucellaceae;
 Bacteria; Proteobacteria;
 RIBH.
126 HDFFH 130
 70 HEFLH
 1 HDFLH 5
 1 HDFLH 5
 n. Diagn. Lab. Immunol. 2:263-267(1995).
FUNCTION: RIBOFLAVIN SYNTHASE IS A BIFUNCTIONAL ENZYME COMPLEX
CATALYZING THE FORMATION OF RIBOFLAVIN FROM 5-AMINO-6-(1'-D)-
 PATHWAY: FINAL STEP OF RIBOFLAVIN SYNTHESIS. SUBUNIT: OLIGOMER THAT CONSIST OF 3 ALPHA SUBUNITS
 RIBOFLAVIN + 4-(1-D-RIBITYLAMINO)-5-AMINO-2,6-DIHYDROXYPYRIMIDINE COFACTOR: FLAVOPROTEIN (BY SIMILARITY).
 4-PHOSPHATE YIELDING 6,7-DIMETHYL-8-LUMAZINE (BY SIMILARITY). CATALYTIC ACTIVITY: 2 6,7-DIMETHYL-8-(1-D-RIBITYL)LUMAZINE -
 RIBITYL-AMINO-2,4(1H,3H)-PYRIMIDINEDIONE AND L-3,4-DIHYDROHY-2-BUTANONE-4-PHOSPHATE VIA 6,7-DIMETHYL-8-LUMAZINE. THE BETA SUBUNIT CAPALYZES THE CONDENSATION OF 5-AMINO-6-(1'-D)-RHBITYL-AMINO-2,4(1H,3H)-PYRIMIDINEDIONE WITH L-3,4-DIHYDROHY-2-BUTANONE-
 Similarity
4; Conser
 Similarity
 74
 biosynthesis;
158 AA; 17356
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 Bioinformatics Institute.
 (BY SIMILARITY).
 Brucella.
 STANDARD;
 PubMed=7664168;
 17356
 87.5%;
 87.5%;
80.0%;
 Transferase; Flavoprotein. 6 MW; EE59C2C815E53A2B CRC64;
 alpha subdivision; Rhizobiaceae group;
 Score 28; Pred. No.
 Score 28;
Pred. No.
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Y038_NPVOP
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 P75288;
01-OCT-2000 (
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 "The sequence of the Orgyia polyhedrosis virus genome." Virology 229:381-399(1997).
 Orgyła pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
 01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 24.3 KDA PROTEIN (ORF22) (ORF 7)
 Q05125; O10283;
01-NOV-1997 (Re
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 SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
This SWISS-PROT entry is copyright. between the Swiss Institute of Bio
 Russell R.L.Q., Rohrmann G.F.;

"Nucleotide sequence of the ubiquitin-39K gene region pseudotsugata multinucleocapsid nuclear polyhedrosis v J. Gen. Virol. 74:1191-1195(1993).
 Ahrens C.H., Russell Rohrmann G.F.;
 SEQUENCE FROM N.A. MEDLINE-97271300; PubMed-9126251;
 01-NOV-1997 (Rel. 01-NOV-1997 (Rel.
 Hypothetical
SEQUENCE 10
 use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
 Mycoplasmataceae; Mycoplasma
NCBI_TaxID=2104;
 Mycoplasma pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 MEDLINE-93286576;
 SEQUENCE OF
 NCBI_TaxID=10450;
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 Nucleic
 pneumoniae."
 Herrmann R.;
 Himmelreich R., Hilbert H.,
 MPN499 OR MP344.
 HYPOTHETICAL PROTEIN MPN499 (P02_ORF163).
 *Complete sequence
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 SIMILARITY: TO CORRESPONDING ORF
 HDFLH
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 AE000032; AAB95991.1;
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 an email to license@isb-sib.ch).
 Acids Res. 24:4420-4449(1996).
 76
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 30-209 FROM N.A.
 (Rel. 35, Created)
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 STANDARD;
 PubMed=8389803;
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 Evans J., Harwood
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 CRC64
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EMBL outstation
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 Mycoplasma
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RESULT
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Best Local 9
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BZTD_RHOCA
Q52666;
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 Hypothetical protein. CONFLICT 35
 Pfam; PF00005; ABC_tran; 1.
PROSITE; PS00211; ABC_TRANSPORTER;
 EMBL; U37407; AAB17889.1; -. InterPro; IPR001617; -.
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
 SEQUENCE FROM N.A.
STRAIN-SB1003 / ST LOUIS;
 BZTD
 GLUTAMATE/GLUTAMINE/ASPARTATE/ASPARAGINE TRANSPORT
 SEQUENCE
 EMBL; U75930; AAC59021.1; EMBL; D13375; BAA02636.1;
 or send an email to license@isb-sib.ch).
 Amino-acid transport;
 "A glutamate/glutamine/aspartate/asparagine transport operon Rhodobacter capsulatus.";
 MEDLINE=96405624; PubMed=8809753;
 NCBI_TaxID=1061;
 Rhodobacter
 Bacteria; Proteobacteria;
 Rhodobacter
 15-JUL-1998
01-OCT-2000
 2neng
 186 HDFFH 190
 1 HDFLH
 FUNCTION: PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM GLUTAMATE, GLUTAMINE, ASPARTATE, ASPARAGINE. PROBABLY RESPONSIB FOR ENERGY COUPLING TO THE TRANSPORT SYSTEM.

SUBUNIT: BZTB AND BZTC FORM A HETERODINER WHICH CAN FORM A MEMBRANE COMPLEX WITH A HOMODIMER OF BZTD (POTENTIAL).

SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED (POTENTIAL).
 European Bioinformatics Institute.
 SIMILARITY:
 European Bioinformatics Institute.
 Microbiol.
 S., Haselkorn R.;
 4
 Similarity
 non-profit institutions as long as its content is in and this statement is not removed. Usage by and for comrequires a license
 TRANSPORTERS).
 G
 209 AA;
 capsulatus (Rhodopseudomonas capsulata).
roteobacteria; alpha subdivision; Rhodobacter group;
 (Rel. 36, Created)
(Rel. 36, Last sequence up
(Rel. 40, Last annotation
 Conservative
 ΑĄ,
 STANDARD;
 BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
 20:1001-1011(1996)
 36 I
24253 MW;
62
30012
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 87.5%;
80.0%;
Transport; ATP-binding.
2 ATP (POTENTIAL).
0012 MW; A08DF5AEB6A4498D
 0;
 Score 28; DB
Pred. No. 31;
 E
 PRT;
 E -> R (IN REF. 2)
C344C51CB9F78D66
 Mismatches
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 Usage
 1;
 Length 209
 CRC64;
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Score 28; DB Pred. No. 40; 0; Mismatches

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 RESULT 11
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 EMBL; U14000,
EMBL; AE000495; AAC//120
EMBL; L06097; AAA24225.1; -
EMBL; EG11402; treC.
TDR000461; -
 Hydrolase;
ACT_SITE
ACT_SITE
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CONFLICT
 EMBL; U06195; AAC43382.1; -. EMBL; U14003; AAA97136.1; -. EMBL; AE000495; AAC77196.1; -.
 "A possible glycine radical in anaerobic ribonucleotide reductase from Escherichia coli: nucleotide sequence of the cloned nrdD gene."; Proc. Natl. Acad. Sci. U.S.A. 90:577-581(1993).
-1- CATALYTIC ACTIVITY: ALPHA, ALPHA-TREHALOSE 6-PHOSPHATE + H(2)0 - D-GLUCOSE + D-GLUCOSE 6-PHOSPHATE.
-1- SUBCELLULAR LOCATION: CYTOPLASMIC.
-1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
 Blattner F.R.;
"Analysis of the Escherichia coli genome region from 92.8 through 100 minutes.";
Nucleic Acids Res. 23:2105-2119(1995).
SEQUENCE
 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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 This
 Sun
 Rimmele M., Boos W.;
"Trehalose-6-phosphate hydrolase of Escherichia
J. Bacteriol. 176:5654-5664(1994).
 P28904;
01-DEC-1992
 Pfam; PF00128; alpha-amylase;
 the European Bioinformatics Institute.
 STRAIN-K12 / W3110;
MEDLINE-93133831; F
 STRAIN=K12 / MG1655;
MEDLINE=95334362; PubMed=7610040;
 SEQUENCE FROM N
 MEDLINE=94364944;
 STRAIN-K12
 SEQUENCE
 Burland V.D., Plunkett G. III, Sofia H.J.,
 Escherichia
 TREC OR OLGH.
 TREHALOSE-6-PHOSPHATE
 Bacteria;
 Escherichia coli
 PHOSPHOTREHALASE).
 30-MAY-2000 (Rel.
 TREC_ECOLI
 Reichard
 EQUENCE FROM N.A
 242
 SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
 HDFFH 246
 Harder J., Krook M.,
 OF 160-392 FROM N.A.
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 Glycosidase.
200 200
251 251
325 325
74 74
 Proteobacteria;
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 STANDARD;
 31, Last sequence update)
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HATE HYDROLASE (EC 3.2.1.93)
 PubMed=8421692;
 PubMed=8083158,
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 gamma subdivision; Enterobacteriaceae;
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 Joernvall H., Sjoeberg B.-M.,
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 Daniels D.L.,
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RESULT 12

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Hydrolase;
ACT_SITE
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 EMBL;
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EMBL;
 alpha(1,1)glucosidase (TreA) of Bacillus subtilis 168.";
J. Bacteriol. 177:2721-2726(1995).
I. CATALYTIC ACTIVITY: ALPHA, ALPHA-TREHALOSE 6-PHOSPHATE + FD-GLUCOSE + D-GLUCOSE 6-PHOSPHATE.
I. SUBCELLULAR LOCATION: CYTOPLASMIC.
I. SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES,
 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 CHARACTERIZATION.
MEDLINE=95270588; PubMed=7751281;
Gotsche S., Dahl M.K.;
 Yamamoto H., Uchiyama S., Sekiguchi J.; "Cloning and sequencing of a 40.6 kb segment in the 73 degrees-76 degrees region of the Bacillus subtilis chromosome containing genes for trehalose metabolism and acetoin utilization.";
 InterPro; IPR000461; -.
Pfam; PF00128; alpha-amylase;
 SubtiList; BG11010; treA.
 HSSP;
 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW
 "Cleavage of trehalose-phosphate in Bacilla phospho-alpha-(1-1)-glucosidase encoded a phospho-alpha-(1-1)-glucosidase encoded Mol. Microbiol. 16:111-120(1995).
 the European Bioinformatics Institute.
 Microbiology 142:3057-3065(1996).
 MEDLINE-97124190; PubMed-8969503;
 STRAIN=168 / MARBURG;
MEDLINE=95379486; PubMed=7651129,
 SEQUENCE FROM N.A
STRAIN=168 / MARBI
 Bacillus/Staphylococcus
NCBI_TaxID=1423;
 Bacteria; Firmicutes;
 TREA OR TREC
 SEQUENCE FROM N.A.
 Bacillus subtilis.
 PHOSPHOTREHALASE).
 *Purification and characterization
 230 HEFLH 234
 1 HDFLH 5
 ; Z54245; CAA91015.1; -..; X80203; CAA56495.1; -..; D83967; BAA23408.1; -..; Z99108; CAB12610.1; -..; P21332; 100K.
 KNOWN AS THE ALPHA-AMYLASE FAMILY.
 4 ;
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 ; Glycosidase.
203 203
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 87.5%;
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HYDROLASE (EC 3.2.1.93)
 Bacillus/Clostridium group;
us group; Bacillus.
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Eldering J.A., Groenberg J., Sterchi E.E.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF PROTEIN AND PEPTII
-!- PREFERENTIALLY ON CARBOXYL SIDE OF HYDROPHOBIC RESII
-!- COFACTOR: BINDS ONE ZINC ION.
-!- SUBUNIT: HOMOTETRAMER OF ALPHA OR BETA SUBUNITS; HE'
-!- OF TWO ALPHA AND TWO BETA SUBUNITS ARE FORMED BY NO
 MEPB_HUMAN STANDARD; PRT; 700 AA. Q16820; Q16820; Q1.00V-1997 (Rel. 35, Created) Q1.00V-1997 (Rel. 35, Last sequence update) Q1-NOV-1997 (Rel. 35, Last annotation update) Q1-NOV-1997 (Rel. 35, Last annotation update) MERTA SUBUNIT PRECURSOR (EC 3.4.24.18) (ENDOPEDTIDASE-2) (N-BENZOYL-L-TYROSYL-P-AMINO-BENZOIC ACID HYDROLASE BETA SUBUNIT) (PABA PEFTIDE HYDROLASE) (PPH BETA).
 ACT_SITE
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 HUMAN
 Pfam;
 MEROPS; M12.002; -. MEROPS; M12.004; -. MIM; 600389; -.
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HSSP; P28825;
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233 HEFLH
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1B (Human),
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 1 HDFLH
 ASSOCIATION OF TWO DISULFIDE-LINKED HETERODIMERS (BY S: SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
SIMILARITY: CONTAINS 1 MAM DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
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 PF01400;
PF00629;
 PF00917;
 Similarity 80.
4; Conservative
 ; IPRO00130; -.; IPRO00561; -.; IPRO00998; -.; IPRO01506; -.; IPRO02083; -.
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 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 12C0AC7F069139A5 CRC64;
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 PRINTS; PRO0480; ASTACIN.
PROSITE; PS00142; ZINC_PRO
PROSITE; PS00740; MAM_1; 1
PROSITE; PS50060; MAM_2; 1
PROSITE; PS00022; EGF_1; F
PROSITE; PS01186; EGF_2; F
 MEPB_MOUSE
Q61847;
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CARBOHYD
 Jenkins N.A., Bond J.S.; "Cloning, expression, and chromosomal localization meprin beta subunit.";
 _MOUSE
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Dietrich J.M., Bond J.S., Jiang W.; "A novel meprin beta' mRNA in mouse carcinoma cells.";
 TISSUE=Kidney;
MEDLINE=96147211; PubMed=8567689;
 TISSUE-Kidney;
MEDLINE-94012651; PubMed-8407940;
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 MEPRIN A BETA-SU
MEP1B OR MEP-1B
 Gorbea C
 SEQUENCE FROM N.A.,
 Mus musculus
 SEQUENCE
 CARBOHYD
 DISULFID
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 SIGNAL
 Zymogen;
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090
 Transmembrane;
 152 HEFLH
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997 (Rel. 35, Last sequence update)
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BETA-SUBUNIT PRECURSOR (EC 3.4.24.
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 EMBL; L15193; HSSP; P28825;
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LYTIC ACTIVITY: HYDROLYSIS OF PROTEIN AND PEPTIDE SUBSTRATES

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Biol. Chem. 268:17647-17647(1993).
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Pfam; PF00629; MAM; 1.
Pfam; PF00917; MATH; 1.
PFINTS; PR00020; MAMDOMAIN.
PRINTS; PR00042; ZINC_PROTEASE; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00740; MAM_1; 1.
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 Score 28; DB 1; L
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|             | ·                   |       | 3            | F., 9 | ,    | 100                                   | ÷        |           |                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |     |          |       |
|             |                     | •     | 8 8          |       |      |                                       | · · ·    |           | *                                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 9   |          |       |
| 1           |                     |       | <u>.</u>     | q     | •    | er.                                   |          |           | •                                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |     |          |       |
| 9           |                     | 1     |              |       |      |                                       |          |           |                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |     |          |       |
|             |                     |       |              |       |      | - :                                   | di S     |           |                                       | •                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |     | * **     | .4    |
| ,           |                     | . ,   | , ,          | , •   |      |                                       | <b>.</b> | ÷         |                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |     |          | -     |
|             |                     |       |              | *     |      | `                                     | 36       |           |                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |     |          |       |
|             |                     | *     |              |       |      |                                       | •        |           |                                       | **                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |     |          |       |
|             |                     | ••*   |              |       | , .  |                                       | ,        |           |                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ,   | *:       |       |
| <b>)</b> ,. |                     |       |              |       |      | e e e e e e e e e e e e e e e e e e e |          |           |                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |     |          | ;     |
|             |                     |       |              |       |      | + 7                                   |          | :         |                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |     |          |       |
| •           |                     |       | S            |       |      |                                       |          | ř         |                                       | · r                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |     |          |       |
| 4."<br>K    |                     | **    |              |       | . ,  |                                       |          |           |                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |     | . 3.     | *     |
|             |                     | à a   |              |       |      | 1. Se e                               | Bear of  |           |                                       | 2 06                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |     | er Prima |       |
| ė,          |                     |       |              | •     |      |                                       | , ·      |           | <i>n</i> ,                            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |     |          |       |
| 1           |                     |       | 3.e          | · .   | •    |                                       | *, *     |           |                                       | т.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | · , | -        |       |
|             |                     |       | • <u>•</u> • |       |      |                                       |          |           |                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |     |          |       |
|             |                     |       | <b>v</b> .,  | NA,   |      |                                       |          |           |                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |     |          |       |
|             |                     |       |              | •     |      | ~                                     |          |           |                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |     |          |       |
|             | •                   |       |              |       |      |                                       |          |           |                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | •   |          |       |
|             |                     |       |              |       |      |                                       |          |           |                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |     |          |       |
|             |                     |       |              |       |      |                                       |          | C.        |                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |     |          |       |
|             |                     |       |              |       |      |                                       |          |           |                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |     |          |       |

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 Total number of hits satisfying chosen parameters:
 Sequence:
 Title:
Perfect score:
 Run
 OM protein - protein search, using sw model
 Database
 Searched:
 Scoring table:
Listing

A_Geneseq_0601:*

1: /SIDS8/gcgdata/
2: /SIDS8/gcgdata
3: /SIDS8/gcgdata
3: /SIDS8/gcgdat
4: /SIDS8/gcgda
5: /SIDS8/gcgda
6: /SIDS8/gcgd
7: /SIDS8/gcgd
8: /SIDS8/gcgd
9: /SIDS8/gcgd
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15: /SIDS8/gcg
16: /SIDS8/gcg
17: /SIDS8/gcg
18: /SIDS8/gcg
19: /SIDS8
 9
9
1: /SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT: *
2: /SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT: *
3: /SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT: *
3: /SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT: *
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7: /SIDSB/gcgdata/geneseq/geneseqp/AA1992.DAT: *
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7: /SIDSB/gcgdata/geneseq/geneseqp/AA1993.DAT: *
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7: /SIDSB/gcgdata/geneseq/geneseqp/AA1995.DAT: *
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7: /SIDSB/gcgdata/geneseq/geneseqp/AA
 412676 seqs, 60623988 residues
 Gapop 10.0 ,
 BLOSUM62
 US-09-367-013B-2_COPY_39_43
 1 KVYDV 5
 August
 Copyright
 9, 2001, 20:24:14;
 GenCore version 4.5 (c) 1993 - 2000 Compugen Ltd.
 Gapext 0.5
 Search time 79.24 Seconds
 (without alignments)
3.825 Million cell updates/sec
 412676
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| 11                 | 10                 | 9                  | 89                 | 7                 | 6                  | S                  | 4                  | ω                  | 2                  | 1                  | Result<br>No.  |   |           |
|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------------|---|-----------|
| 26                 | 26                 | 26                 | 26                 | 26                | 26                 | 26                 | 26                 | 26                 | 26                 | 26                 | Score          |   |           |
| 100.0              | 100.0              | 100.0              | 100.0              | 100.0             | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | Query<br>Match | œ |           |
| 120                | 116                | 104                | 104                | 104               | 96                 | 95                 | 90                 | 79                 | 78                 | 60                 | Length         |   |           |
| 21                 | 21                 | 21                 | 21                 | 21                | 21                 | 21                 | 21                 | 21                 | 21                 | 21                 | DB             |   |           |
| AAB11409           | AAG32671           | · AAG44772         | AAG18358           | AAB24812          | AAG28353           | AAG19062           | AAG38087           | AAG35333           | AAG27099           | AAG18359           | ID             |   | SUMMARIES |
| S. cerevisiae cyto | Zea mays protein f | Arabidopsis thalia | Arabidopsis thalia | Plant SDF encoded | Arabidopsis thalia | Zea mays protein f | Arabidopsis thalia | Zea mays protein f | Zea mays protein f | Arabidopsis thalia | Description    |   | 2S        |

| 45                 | 44                 | 43                 | 42                | 41       | 40                 | 39       | 38       | 37       | 36                 | 35                 | 34       | ω<br>ω   | 32                | 31                 | 30                 | 29                 | 28                 | 27       | 26                 | 25       | 24                | 23                | 22                | 21       | 20                 | 19                | 18                 | 17                 | 16                 | 15                 | 14       | 13  | 12                 |
|--------------------|--------------------|--------------------|-------------------|----------|--------------------|----------|----------|----------|--------------------|--------------------|----------|----------|-------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|----------|-------------------|-------------------|-------------------|----------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|----------|-----|--------------------|
| 26                 | 26                 | 26                 | 26                | 26       | 26                 | 26       | 26       | 26       | 26                 | 26                 | 26       | 26       | 26                | 26                 | 26                 | 26                 | 26                 | 26       | 26                 | 26       | 26                | 26                | 26                | 26       | 26                 | 26                | 26                 | 26                 | 26                 | 26                 | 26       | 26  | 26                 |
| 100.0              |                    |                    | 100.0             |          | 100.0              |          |          |          |                    |                    |          |          |                   | •                  |                    |                    |                    | •        |                    | 100.0    | 100.0             | 100.0             |                   |          |                    |                   |                    |                    | 100.0              |                    | 100.0    |     | 100.0              |
| 428                | 426                | 425                | 410               | 377      | 349                | 325      | 325      | 254      | 254                | 241                | 200      | 195      | 195               | 181                | 166                | 164                | 155                | 151      | 151                | 151      | 151               | 151               | 151               | 146      | .140               | 140               | 138                | 136                | 136                | 135                | 134      | 129 | 126                |
| 19                 | 19                 | 19                 | 19                | 20       | 20                 | 21       | 21       | 22       | 19                 | 21                 | 21       | 21       | 21                | 21                 | 21                 | 21                 | 21                 | 21       | 21                 | 21       | 21                | 21                | 21                | 21       | 21                 | 21                | 21                 | 21                 | 21                 | 21                 | 21       | 21  | 21                 |
| AAW46963           | AAW46961           | AAW46962           | AAW41059          | AAY09306 | AAY09298           | AAG46647 | AAG28976 | AAB50617 | AAW41987           | AAG54931           | AAG54881 | AAG44771 | AAB24811          | AAG38086           | AAG28351           | AAY44213           | AAG38571           | AAG38091 | AAG34247           | AAB24941 | AAB24830          | AAB24809          | AAB24761          | AAG34407 | AAG37798           | AAB24685          | AAG28352           | AAG34993           | AAG07764           | AAG23317           | AAG07989 | Ç   | AAG23318           |
| Amino acid sequenc | Amino acid sequenc | Amino acid sequenc | Phytoene synthase | Gns9     | Rice beta-glucanas | S        | ĺS       | a        | Flea serine protea | Arabidopsis thalia | S        | S        | Plant SDF encoded | Arabidopsis thalia | Arabidopsis thalia | Rice phytoene synt | Arabidopsis thalia | S        | Arabidopsis thalia |          | Plant SDF encoded | Plant SDF encoded | Plant SDF encoded | S        | Arabidopsis thalia | Plant SDF encoded | Arabidopsis thalia | Arabidopsis thalia | Arabidopsis thalia | Arabidopsis thalia | ìs       | S   | Arabidopsis thalia |

## ALIGNMENTS

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RESULT
AAG18359
 25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

25-MAR-1999

01-APR-1999

01-APR-1999

08-APR-1999

16-APR-1999

19-APR-1999

21-APR-1999
 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
 Arabidopsis thaliana protein fragment SEQ ID NO: 19732.
 06-SEP-2000.
 Arabidopsis thaliana
 17-OCT-2000
 AAG18359;
 AAG18359 standard; Protein;
 25-FEB-2000;
 EP1033405-A2
 termination sequence
 ш
 (first entry)
 2000EP-0301439
99US-0121825.
99US-012548.
99US-0125548.
99US-0125788.
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99US-0126785.
99US-0127462.
99US-0128714.
99US-0128714.
99US-0128075.
99US-0130077.
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                                                                       | ו סי טי                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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                                                                       | ייטריטיטיטיטיטיטיטיטיטיטיטיטיטיטיגיג<br>געת א א א א א א א א א א א א א א א א א א א                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               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Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;

pathway;
promoter;

Arabidopsis thaliana protein fragment SEQ ID NO: 19731.

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 The present invention describes polynucleotides, such as complete cDNA sequences and/or sequences of genomic DNA encompassing complete genes, portions of genes, and/or intergenic regions, collectively referred to as sequence-determined DNA fragments (SDFs), from corn plants and Arabidopsis thaliana. The SDFs are promoters, structural genes, untranslated regions (UTRs), or 3' termination sequences. They can be used for expressing a gene product and controlling expression of a target gene, either as a promoter, a structural gene, an UTR or as a 3' termination sequence. They are also useful as tools for genetic mapping, and identification of a particular individual plant or for clustering a group pf plants with a common trait. AAA78433 to AAA78630 and AAB24605 to AAB25099 represent the specifically claimed polynucleotide sequences and polypeptides encoded by them given in the
 Claim 14; Page 464; 673pp; English.
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 13-JUL-2000
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 27 - NOV - 2000
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 New corn plant and Arabidopsis thaliana sequence-determined DNA fragments, useful for expressing gene products and for controlling
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RESULT 1
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 08-OCT-1999;
12-OCT-1999;
13-OCT-1999;
13-OCT-1999;
 Nucleic acid sequences cytochrome b5 and used
 Cytochrome b5; alkane metabolism; oxidation; long-chain alkyl compound; long-chain dicarbonic acid.
 WPI; 2000-679674/66
 18-APR-2000; 2000WO-DE01246.
 02-NOV-2000
 WO200065061-A2
 Saccharomyces cerevisiae.
 S. cerevisiae cytochrome b5 protein
 22-FEB-2001 (first entry)
 AAB11409 standard; Protein; 120 AA.
 14-OCT-1999;
14-OCT-1999;
 24-APR-1999;
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990S-0160815

990S-0160815

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990S-0160981

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990S-0161361

 99DE-1018763
 100.0%;
 159295
 from alkane metabolizing Candida yeast, encoding for the oxidation of long chain alkyl compounds of long chain dicarbonic acids -
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 Score 26;
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Mismatches
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Query Match
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25-MAR 1999
01-APR 1999
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11-APR 1999
23-APR 1999
24-MAY 1999
30-APR 1999
30-APR 1999
31-APR 1999
 This invention describes novel nucleic acid sequences from alkane metabolizing Candida yeasts, encoding cytochrome b5-polypeptide, its fragments, variants and mutations. The nucleic acids and polypeptides are used for the oxidation of long-chain alkyl compounds with at least 10C, and for the production of long-chain dicarbonic acids by oxidizing n-alkanes and fatty acids with at least 10C.
 06-SEP-2000
 Arabidopsis thaliana
 Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
 Arabidopsis thaliana protein fragment SEQ ID
 17-OCT-2000
 AAG23318;
 AAG23318 standard; Protein; 126
 Sequence
 25-FEB-2000;
 EP1033405-A2
 termination sequence.
 Example 1.4; Fig 2A;
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| 26 kvydv 30
 1 KVYDV 5
 5.
 Similarity
 120
 Conservative
 (first entry)
 2000EP-0301439
990S-0128234

990S-0128714

990S-0129045

990S-0130077

990S-0130510

990S-0130891

990S-013248

990S-013248

990S-0132485

990S-0132485

990S-0132486

990S-0132863

990S-013428

990S-013425

990S-013421

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 Total number of hits satisfying chosen parameters:
 Title:
Perfect score:
 Result
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Sequence 3, Appli
Sequence 4, Appli
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Sequence
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| Appli           | Appli           | Appl              | Appl              | Appl              | Appli           | Appli           | Appl             | App1             | Appli           | Appl             | Tddv             |

## ALIGNMENTS

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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: 24-APR-1996
ATTORNEY/ACENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/JOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
THIFFAX: (303) 863-9700
 TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 GENERAL INFORMATION: APPLICANT: Grieve.
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
 APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
APPLICANT: Silver, Gary
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
 CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES:
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
 CITY: Denver
STATE: Colorado
 TOPOLOGY: linear
 COUNTRY:
 STREET:
 LENGTH:
 ADDRESSEE:
 80203
 79, Application US/08906769
6077687
 amino acids
 1700 Lincoln Street, Suite 3500
 USA
 Grieve, Robert
Rushlow, Keith
 Grieve,
 Sheridan Ross & McIntosh
 protein
 190
 2618-25-C2
 Version #1
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Q
 ; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-906-616-129
 US-08-639-075A-129
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 Query Match
Best Local Similarity
Thes 5; Conserve
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 Qγ
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Best Local Similarity
Thes 5; Conserve
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 Sequence 129, Application US/08639075A Patent No. 6150125
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 Patent No.
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FILING DATE: 05-AUG-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
 GENERAL INFORMATION:
 TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO:
 APPLICANT:
APPLICANT:
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 SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acid
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 APPLICANT:
 APPLICANT:
 MEDIUM TYPE: Floppy disk
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 COUNTRY:
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 CITY:
 88 KVYDV 92
 ADDRESSEE:
 1 KVYDV 5
 1 KVYDV 5
 80203
 Denver
 Colorado
 1700 Lincoln Street,
Grieve, Robert B.
Rushlow, Keith E.
Wu Hunter, Shirley
Frank, Glenn R.
 100.0%; Score 26; DE nilarity 100.0%; Pred. No. 60; Conservative 0; Mismatches
 100.0%; Score 26; DB illarity 100.0%; Pred. No. 60; Conservative 0; Mismatches
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VENTION: FLEA AMINOPEPTIDASE PROTEINS AND USES THEREOF
 Stiegler, Gary
 Gaines, Patrick J.
 Frank, Glenn R.
 Wu Hunter, Shirley
 Grieve, Robert B. Rushlow, Keith E.
 3 ADDRESS:
Sheridan Ross P.C.
Sheridan Ross P.C.
Sheridan Ross P.C.
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 REGISTRATION NUMBER: 32,020
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TELEPHONE: (303) 863-9700
 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
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 88 KVYDV 92
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 COUNTRY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
 APPLICANT: Grieve, Robert B.
Rushlow, Keith E.
Wu Hunter, Shirley
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
 TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
 NUMBER OF SEQUENCES: 190
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 STATE: Colorado
 CITY: Denver
 Colorado
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1700 Lincoln Street, Suite 3500
 100.0%; ilarity 100.0%; Conservative
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 Gaines, Patrick J.
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 Gaines, Patrick J.
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Pred. No.
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NUMBER OF SEQUENCES:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS'
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 FILING DATE:
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 COUNTRY:
 ADDRESSEE:
 88 KVYDV 92
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 ATTORNBY/AGENT INFORMATION:
NAME: CONNELL, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
TELEFOME: (303) 863-9700
TELEFAX: (303) 863-9700
TELEFAX: (303) 863-0223
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 Frank, Glenn R.
Stiegler, Gary
 Silver, Gary
 Gaines, Patrick J.
 Wu Hunter, Shirley
 Grieve, Robert B. Rushlow, Keith E.
 Sheridan Ross & McIntosh
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ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 26.8
TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 863-971
TELEFAX: (303) 863-0223
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CITY: Denver
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 Gaines, Patrick J.
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 Stiegler, Gary
 Rushlow, Keith E. Wu Hunter, Shirley
 Frank, Glenn R.
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100.0%; Pred. No.
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 2618-25-C2
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88 KVYDV 92

1 KVYDV 5

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 US-08-834-655-2
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 ; MOLECULE TYPE: protein US-08-579-667-6
 US-08-579-667-6
Patent No. 5900007

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KUUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: HUANG, JENNIEER
APPLICANT: CHAUDHARY, SUNITA
APPLICANT: CHAUDHARY, SUNITA
ITITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
ITITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
ITITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 Sequence 2, Application US/08834655 Patent No. 5968809
 Sequence be Patent No.
 TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO:
 ZIP: 28234

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 APPLICANT:
APPLICANT:
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TYPE: amino acid
TOPOLOGY: linco
 SEQUENCE CHARACTERISTICS:
 REFERENCE/DOCKET NUMBER: 62
TELECOMMUNICATION INFORMATION: 919-420-2200
 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/579,667
 CORRESPONDENCE ADDRESS:
 APPLICANT: Kumagai, Monto H.
APPLICANT: Della-Cioppa, Guy R.
TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN
TITLE OF INVENTION: PHYTOENE BIOSYNTHESIS
 NUMBER OF SEQUENCES:
 78 KVYDV 82
 NAME: Bennett, Virginia C. REGISTRATION NUMBER: 37,092
 FILING DATE:
 COUNTRY:
 STATE:
 ADDRESSEE:
 1 KVYDV 5
 INFORMATION:
 6, Application US/08579667
5, 5705624
 Charlotte : No. 5705624th Carolina
 E: Virginia C. Bennett
1211 East Morehead Street,
 USA
 Hellmann, Gary M. Grill, Laurence K.
 Conservative
 Fitzmaurice, Wayne P.
 100.0%; Score 26; DB 100.0%; Pred. No. 99;
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 627-196
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 DB 1; Length 410;
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 US-08-834-655-2
 Sequence 4 Patent No.
 Matches
 Query Match
Best Local
 INFORMATION FOR SEQ ID NO:
 APPLICANT:
APPLICANT:
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 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-BOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,610
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
 CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVE, P.O. BOX 60039
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
 SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
 ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGN
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 APPLICANT:
 MOLECULE TYPE:
 CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFORMATION:
 NUMBER OF SEQUENCES:
 STREET: 260 SHER
CITY: PALO ALTO
 39 KVYDV 43
 Local Similarity
nes 5; Conserv
 COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patentl
 STREET: 260 SHE
CITY: PALO ALTO
STATE: CA
 ZIP: 94306
 COUNTRY:
 STATE:
 STRANDEDNESS:
TOPOLOGY: lin
 CLASSIFICATION:
 COUNTRY: UP ZIP: 94306
 ADDRESSEE: RAE-VENTER LAW GROUP, P.C. STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
 1 KVYDV 5
 4, Application US/08833610
p. 5972664
 INFORMATION:
 amino acid
 CALIFORNIA
 MURKERJI, PRADIP
HUANG, YUNG-SHENG
THURMOND, JENNIFER
CHAUDHARY, SUNITA
 100.0%; Score 26; DB 2; illarity 100.0%; Pred. No. 1.le+02; Conservative 0; Mismatches 0;
 USA
 USA
 KNUTZON, DEBORAH
 PatentIn Release #1.0, Version #1.30
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 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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 Gaps
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RAE-VENTER, BARBARA

CGNE.123.00US

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Query Match
Best Local Similarity
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 US-08-834-033A-2
 US-08-833-610-4
 Sequence 2, Application US/08834033A Patent No. 6075183
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
 GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
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INFORMATION FOR SEQ ID NO: 2:
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
 STRANDEDNESS: not rel
TOPOLOGY: linear
MOLECULE TYPE: peptide
 REGISTRATION NUMBER: 32,750
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)328-4400
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LENGTH: 457 amino acids
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 APPLICANT: MUKERJI PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURNOND, JERNIFER
APPLICANT: CHAUDHARY, SUNITA
MOLECULE TYPE: peptide
 TELEFAX: (v
 TOPOLOGY:
 STRANDEDNESS:
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1
 STREET: ZUVI. ... CITY: SAN FRANCISCO
 39 KVYDV 43
 COUNTRY:
 TELEFAX:
 1 KVYDV 5
 94111
 amino acid
 amino acid
 USA
 (415) 433-8716
 Conservative
 KNUTZON, DEBORAH
 (650)328-4477
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US-09-363-574-2
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US-08-834-033A-14
 Sequence 2, Application US/09363574
Patent No. 6136574
 Patent No.
 Sequence 14,
 Query Match
Best Local Similarity
 Matches
 GENERAL INFORMATION:
 APPLICATION NUMBER: US/08/834
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
 TELEX: N/A
INFORMATION FOR SEQ ID NO:
 GENERAL INFORMATION:
 APPLICANT: KNUTZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
 SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
 APPLICANT:
 SEQUENCE CHARACTERISTICS:
 CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 NUMBER OF SEQUENCES:
 MEDIUM TYPE: Floppy also COMPUTER: IBM PC COMPUTER: COMPOZING-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING ANOPODERFECT 5.1
 STREET: 2001 FERRY I
CITY: SAN FRANCISCO
STATE: CA
 39 KVYDV 43
 39 KVYDV 43
 STRANDEDNESS:
 TELEFAX:
 COUNTRY:
 ADDRESSEE: LIMBACH AND LIMBACH, L.L.P. STREET: 2001 FERRY BUILDING
 LENGTH:
 1 KVYDV 5
 1 KVYDV 5
 94111
 $, Application US/08834033A
6075183
 amino acid
 457 amino acids
 USA
 (415) 433-8716
KNUTZON, DEBORAH
MURKERJI, PRADIP
HUANG, YUNG-SHENG
 Conservative
 Conservative
 linear
 peptide
 not relevant
 100.0%;
 100.0%; Score 26; DB 3; 100.0%; Pred. No. 1.1e+02;
 26
 US/08/834,033A
 14:
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 CGAB-300.USA
 Score 26; DB 3; Pred. No. 1.1e+02; Mismatches 0;
 Mismatches
 Length 457;
 Length 457;
 Indels
 0,:
 0;
 Gaps
 Gaps
 0
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밁
 Q
 US-07-749-541A-5
 ; MOLECULE TYPE: peptide US-09-363-574-2
 Sequence 5, Application US/07749541A Patent No. 5317009 GENERAL INFORMATION:
 Query Match
Best Local Similarity
 Matches
 INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
 APPLICANT: Huang, Paul L.
APPLICANT: Huang, Philip L.
APPLICANT: Huang, Philip L.
APPLICANT: Huang, Peter
APPLICANT: Huang, Peter
APPLICANT: Huang, Henry I.
APPLICANT: Chen, Hao-Chia
TITLE OF INVENTION: DNA CODING THEREFOR AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
 STREET: 41
STREET: Washington
CITY: Washington
STATE: DC
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
 REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/363,574
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,6
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 APPLICANT:
 APPLICANT:
 COUNTRY: US
ZIP: 20004
 TYPE: amino acid
STRANDEDNESS: not
 STREET: 2001 FERRY I
CITY: SAN FRANCISCO
STATE: CA
 39 KVYDV 43
 TELEFAX:
 FILING DATE:
 TOPOLOGY:
 CLASSIFICATION:
 COUNTRY:
 ADDRESSEE:
 1 KVYDV 5
 94111
 E: LIMBACH AND LIMBACH L.L.P. 2001 FERRY BUILDING
 (415) 433-8716
 USA
 THURMOND, JENNIFER CHAUDHARY, SUNITA
 Kung, Hsiang-fu
 Conservative
 ...: not relevant
linear
 Lee-Huang, Sylvia
 100.0%; Score 26; DB 4; 100.0%; Pred. No. 1.1e+02;
 CGAB-202 USA
 0;
 Mismatches
 Length 457;
 Indels
 0;
 0;
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В
 RESULT 14
US-08-277-283-1
 ; NAME/KEY: MAP 30 US-07-749-541A-5
 Sequence 1, Apprix
Sequence 1, Apprix
No. 5484889
 Matches
 Query Match
Best Local Similarity
 GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
 APPLICANT:
APPLICANT:
 SOFTWARE: Patentin Release #1.U, VGURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/749,541A
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
FILING DATE: 10/09/90
 SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
 NAME: Livnat, Shmuel REGISTRATION NUMBER: 33,949 REFERENCE/DOCKET NUMBER: LEFTELECOMMUNICATION INFORMATION:
 ATTORNEY/AGENT INFORMATION:
NAME: Livnat, Shmuel
 CURRENT APPLICATION DATA:
 ADDRESSEE: Browdy and Neimark
 TITLE OF INVENTION: A Plant Protein Useful for Treating Tumors TITLE OF INVENTION: and HIV Infection
 APPLICANT:
APPLICATION NUMBER: US 0 FILING DATE: 19-APR-1993 ATTORNEY/AGENT INFORMATION:
 FEATURE:
 MOLECULE TYPE: protein
 NUMBER OF SEQUENCES:
 APPLICANT:
 APPLICANT:
 APPLICANT:
 APPLICANT:
 STATE: DC
COUNTRY: US
ZIP: 20004
 STREET: 419 Seven
 APPLICATION NUMBER: US/08/277,283 FILING DATE:
 30 KVYDI 34
 FILING DATE:
CLASSIFICATION:
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn_Release #1.0, Version #1.25
 CLASSIFICATION: 435
 STRANDEDNESS:
 TOPOLOGY:
 TELEPHONE:
 1 KVYDV 5
 Application US/08277283
 AMINO ACID
 419 Seventh Street, N.W.
 Huang, Henry I.
Huang, Paul L.
 USA
 (202)628-5197
(202)737-3528
OR SEQ ID NO: 5:
 Chen, Hao-CIIIa
Kung, Hsiang-fu
 Conservative
 linear
 Nara, Peter L.
 Huang, Peter
 Huang, Philip L.
 ee-Huang, Sylvia
 96.2%;
80.0%;
 US 08/048,066
 07/594,156
 Score 25;
Pred. No.
 LEE-HUANG=3
 Mismatches
 Length 44;
 Indels
 0
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33,949

0;

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 ; MOLECULE TYPE: protein US-08-277-283-1
 RESULT 15
US-09-098-900-4
 TELEFAX: (202)72-3528
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
 Sequence 4, Application US/09098900 Patent No. 5919629 GENERAL INFORMATION:
 Query Match 96.3
Best Local Similarity 80.0
Matches 4; Conservative
 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
 TYPE: amino acids
STRANDEDNESS: Single
TOPOLOGY: line-
 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,900
FILING DATE:
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: LE
TELECOMMUNICATION INFORMATION:
IMMEDIATE SOURCE:
LIBRARY: GenBa
CLONE: 406602
 CORRESPONDENCE ADDRESS
 APPLICANT: Hillman, Jennifer L. APPLICANT: Goli, Surya K.
 TITLE OF INVENTION: NOVEL HUMAN CLATHRIN-ASSOCIATED TITLE OF INVENTION: PROTEIN
 NUMBER OF SEQUENCES:
 30 KVYDI 34
 STREET: 3174 POI
CITY: Palo Alto
STATE: CA
 COUNTRY: U
 TELEPHONE:
 ADDRESSEE:
 1 KVYDV 5
 E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
 US
 GenBank
 (202)628-5197
 96.2%;
80.0%;
 08/806,877
 PF-0219 US
 LEE-HUANG-1
 Score 25; DB 1;
Pred. No. 16;
1; Mismatches
 0;
 Length 44;
 Indels
 0,
 Gaps
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Query Match

96.2%;

Score 25;

DB 2;

Length 156;

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Ъ
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 Best Local Similarity 80.0%; Pred. No. 62; Matches 4; Conservative 1; Mismatches
112 KVYDI 116
 1 KVYDV 5
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 Indels
 0;
 Gaps
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Search completed: August Job time: 205 sec 9, 2001, 20:25:06

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